

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 2, 2004, 16:26:08 ; Search time 39 Seconds
(without alignments)
2507.965 Million cell updates/sec

Title: US-10-036-150-45

Perfect score: 1617

Sequence: 1 MRLSGGFATCCVAIEVLGI.....LISSAFERKGDIRHPKHVQ 310

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp Vertebrate:*

14: sp_undefined:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1617	100.0	975	4 Q8NCC9	Q8NCC9 homo sapien
2	1156	71.5	299	4 Q8N866	Q8N866 homo sapien
3	1156	71.5	894	4 Q8NC14	Q8NC14 homo sapien
4	878	41.9	1734	5 Q86115	Q86115 dictyostell
5	595	36.8	860	3 Q86X26	Q86X26 yarrowia li
6	590	36.5	897	10 Q8SUY2	Q8SUY2 arabidopsis
7	583	36.1	892	3 Q8TGB2	Q8TGB2 candida alb
8	524	32.4	795	5 Q19870	Q19870 caenorhabdi
9	511.5	31.6	927	5 Q9V4N0	Q9V4N0 drosophila
10	511	31.6	333	6 Q8GM09	Q8GM09 macaca fasc
11	471	29.1	692	10 Q8LNL1	Q8LNL1 cryza sativ
12	421.5	26.1	1077	5 Q7YU86	Q7YU86 drosophila
13	418.5	25.9	1077	5 Q9V8H8	Q9V8H8 drosophila
14	415.5	25.7	884	10 Q9FF16	Q9FF16 arabidopsis
15	414	25.6	918	3 Q13663	Q13663 schizosacch
16	387	23.9	1017	3 Q07830	Q07830 saccharomyc

17	347.5	21.5	901	5	Q01966	O01966 caenorhabdi
18	287.5	17.8	1283	5	Q81SR4	Q81SR4 plasmodium
19	248	15.3	729	5	Q8SV36	Q8SV36 encephalito
20	190.5	11.8	921	10	Q9SGH9	Q9SGH9 arabidopsis
21	176.5	10.9	894	5	Q9V5F7	Q9V5F7 drosophila
22	172.5	10.7	935	3	Q8WZK2	Q8WZK2 schizosacch
23	164.5	10.2	931	4	Q8TC01	Q8TC01 homo sapien
24	164.5	10.2	931	4	Q95427	Q95427 homo sapien
25	163.5	10.1	269	16	Q9PPH8	Q9PPH8 campylobact
26	162.5	10.0	391	11	Q9R1S1	Q9R1S1 mus musculu
27	162.5	10.0	826	11	Q8VCC3	Q8VCC3 mus musculu
28	161.5	10.0	798	11	Q9R1S2	Q9R1S2 mus musculu
29	161.5	10.0	931	11	Q9R1S3	Q9R1S3 mus musculu
30	157	9.7	269	16	Q9HY99	Q9HY99 pseudomonas
31	152.5	9.4	429	2	Q69013	Q69013 zymomonas m
32	151	9.3	485	3	Q94323	Q94323 schizosacch
33	151	9.3	906	5	Q9N3C5	Q9N3C5 caenorhabdi
34	150	9.3	432	16	Q8R1S1	Q8R1S1 xanthomonas
35	147	9.1	479	10	Q42374	Q42374 cryza sativ
36	139	8.6	424	16	Q8P7F7	Q8P7F7 xanthomonas
37	139	8.6	461	10	Q9S081	Q9S081 arabidopsis
38	138.5	8.6	440	11	Q8BGN3	Q8BGN3 mus musculu
39	138	8.5	274	16	Q87JA0	Q87JA0 vibrio para
40	138	8.5	477	4	Q9UJA9	Q9UJA9 homo sapien
41	135	8.3	457	10	Q84WJ3	Q84WJ3 arabidopsis
42	134	8.3	457	10	Q9S082	Q9S082 arabidopsis
43	134	8.3	496	10	Q9S083	Q9S083 arabidopsis
44	132	8.2	540	2	Q84EY0	Q84EY0 fluoribacte
45	130	8.0	271	17	Q8TLV7	Q8TLV7 methanosarc
46	130	8.0	477	11	Q921P7	Q921P7 mus musculu
47	130	8.0	477	11	Q92QG7	Q92QG7 mus musculu
48	130	8.0	479	10	Q9FS13	Q9FS13 spinacia ol
49	127	7.9	440	4	Q96M57	Q96M57 homo sapien
50	122.5	7.6	451	16	Q9A8S4	Q9A8S4 caulobacter
51	122	7.5	433	16	Q9PAB9	Q9PAB9 xyliella fas
52	119	7.4	433	16	Q9A8S5	Q9A8S5 xyliella fas
53	118.5	7.3	179	3	Q9US89	Q9US89 schizosacch
54	118	7.3	278	16	Q88W49	Q88W49 pseudomonas
55	118	7.3	963	11	Q7ZKN7	Q7ZKN7 xenopus lae
56	118	7.3	963	11	Q811J3	Q811J3 mus musculu
57	114	7.1	370	17	Q58841	Q58841 pyrococcus
58	113.5	7.0	662	16	Q89P20	Q89P20 pseudomonas
59	111.5	6.9	369	17	Q9UZM7	Q9UZM7 pyrococcus
60	111.5	6.9	906	11	Q924C4	Q924C4 mus musculu
61	111	6.9	374	17	Q8U205	Q8U205 pyrococcus
62	110.5	6.8	434	16	Q97LS7	Q97LS7 clostridium
63	110	6.8	315	17	Q8TW71	Q8TW71 methanopyru
64	109	6.7	589	10	Q8VXX5	Q8VXX5 arabidopsis
65	108.5	6.7	520	16	Q9CKK7	Q9CKK7 bacillus ha
66	108.5	6.7	550	2	Q55320	Q55320 synschocec
67	108	6.7	919	5	Q9VCV7	Q9VCV7 drosophila
68	106.5	6.6	305	16	Q8A3D1	Q8A3D1 bacteroides
69	106	6.6	287	16	Q87YC2	Q87YC2 pseudomonas
70	105	6.5	272	17	Q8PES5	Q8PES5 methanosarc
71	105	6.5	932	5	Q8IH66	Q8IH66 drosophila
72	104.5	6.5	637	5	Q9BPN8	Q9BPN8 caenorhabdi
73	104	6.4	298	16	Q9SCJ8	Q9SCJ8 rhizobium 1
74	102.5	6.3	548	2	Q9RW11	Q9RW11 neisseria m
75	101.5	6.3	415	11	Q8CAF0	Q8CAF0 mus musculu
76	100.5	6.2	364	5	Q9GR18	Q9GR18 caenorhabdi
77	100.5	6.2	543	16	Q7UFG7	Q7UFG7 rhodospirill
78	98.5	6.1	506	16	Q8EW33	Q8EW33 mycoplasma
79	97.5	6.0	429	16	Q8G4F1	Q8G4F1 bifidobacte
80	97.5	6.0	537	16	Q8XS42	Q8XS42 ralstonia s
81	97.5	6.0	817	12	Q9J5H1	Q9J5H1 fowlpox vir
82	97.5	6.0	817	12	Q90761	Q90761 fowlpox vir
83	97	6.0	207	16	Q8NMW2	Q8NMW2 corynebacte
84	97	6.0	382	2	Q52580	Q52580 comamonas t
85	96.5	6.0	2109	12	Q98776	Q98776 vesicular s
86	96.5	6.0	2109	12	Q86125	Q86125 vesicular s
87	96.5	6.0	2109	12	Q8B010	Q8B010 vesicular s
88	96	5.9	355	16	Q7UMG9	Q7UMG9 rhodospirill
89	96	5.9	510	16	Q87T83	Q87T83 vibrio para

90	96	5.9	561	10	Q9SB39	Q9B39 arabidopsis	163	88	5.4	660	16	Q82795	Q82795 salmonella
91	96	5.9	1840	3	Q9HED6	Q9hed6 neurospora	164	88	5.4	660	16	Q83T27	Q83t27 salmonella
92	96	5.9	2109	12	Q8BOH5	Q8boh5 vesicular s	165	87.5	5.4	385	2	P94599	P94599 bacillus th
93	96	5.9	2163	5	Q9NPE6	Q9npe6 plasmodium	166	87.5	5.4	413	16	Q8L195	Q8l195 bacillus an
94	95.5	5.9	532	16	Q9DBA4	Q9dba4 streptomyce	167	87.5	5.4	465	4	Q8NENA	Q8nb4 lactococcus
95	95.5	5.9	566	16	Q8D7J1	Q8d7j1 vibrio vuln	168	87.5	5.4	488	2	Q9RAT4	Q9rat4 lactococcus
96	96	5.9	311	5	Q9BLZ3	Q9blz3 renilla mue	169	87.5	5.4	1253	5	Q8WQ61	Q8wq61 drosophila
97	95	5.9	411	2	Q7WUC4	Q7wuc4 escherichia	170	87	5.4	220	10	Q9RP70	Q9rp70 oryza sativ
98	93.5	5.8	542	17	Q8PR07	Q8prq7 methanosarc	171	87	5.4	233	10	Q84L55	Q84l55 oryza sativ
99	93.5	5.8	596	16	Q8SP27	Q8sp27 shewanella	172	87	5.4	304	5	Q7Y157	Q7y157 cryptospori
100	92.5	5.8	1480	10	Q7X1J7	Q7x1j7 oryza sativ	173	87	5.4	395	13	Q919T6	Q919t6 lagopus mut
101	92.5	5.7	236	16	Q8ZNR7	Q8znm7 streptomyce	174	87	5.4	423	17	Q97C46	Q97c46 thermoplas
102	92.5	5.7	542	17	Q8TRQ2	Q8trq2 methanosarc	175	87	5.4	459	4	Q96S34	Q96s34 homo sapien
103	92	5.7	318	13	Q90XA9	Q90xa9 xenopus lae	176	87	5.4	488	5	Q9N922	Q9n922 drosophila
104	92	5.7	320	13	Q13026	Q13026 xenopus lae	177	87	5.4	599	16	Q92RD6	Q92rd6 rhizobium m
105	92	5.7	461	16	Q9BQL5	Q9bql5 mycoplasma	178	87	5.4	634	6	Q46600	Q46600 bos taurus
106	91.5	5.7	314	5	Q86D20	Q86d20 caenorhabdi	179	87	5.4	833	5	Q8F1F0	Q8f1f0 trypanosoma
107	91.5	5.7	477	4	Q86VC5	Q86vc5 homo sapien	180	87	5.4	2182	5	Q8I1Z5	Q8i1z5 plasmodium
108	91.5	5.7	503	16	Q7UG72	Q7ug72 rhodospirell	181	86.5	5.3	323	16	Q8F921	Q8f921 leptospira
109	91.5	5.7	542	17	Q8TRV9	Q8trv9 methanosarc	182	86.5	5.3	335	16	Q8PG38	Q8pg38 xanthomonas
110	91.5	5.7	542	17	Q8TQB9	Q8tqb9 methanosarc	183	86.5	5.3	390	5	Q9VA28	Q9va28 drosophila
111	91.5	5.7	542	17	Q8TH47	Q8th47 methanosarc	184	86.5	5.3	424	5	Q8IHE4	Q8ihe4 drosophila
112	91.5	5.7	653	16	Q9PMW6	Q9pmw6 campylobact	185	86.5	5.3	478	16	Q9L109	Q9l109 streptomyce
113	91.5	5.7	1232	5	Q8WMD2	Q8wmd2 drosophila	186	86.5	5.3	500	16	Q9RXX6	Q9rx6 streptomyce
114	91.5	5.7	1233	5	Q9H111	Q9h111 drosophila	187	86.5	5.3	527	16	Q8X7U5	Q8x7u5 escherichia
115	91	5.6	421	17	Q9H1J0	Q9h1j0 thermoplas	188	86.5	5.3	527	16	Q8FVL9	Q8fjl9 escherichia
116	90.5	5.6	217	2	Q8GNK7	Q8gnk7 mycobacteri	189	86.5	5.3	528	16	Q9CP39	Q9cp39 pasteurella
117	90.5	5.6	237	16	Q93VR3	Q93vr3 staphylococ	190	86.5	5.3	1005	5	Q9GR06	Q9gr06 plasmodium
118	90.5	5.6	310	2	Q87616	Q87616 pseudomonas	191	86.5	5.3	1005	5	Q8IBE5	Q8ieb5 plasmodium
119	90.5	5.6	327	16	Q92U57	Q92u57 rhizobium m	192	86	5.3	291	16	Q82KU2	Q82ku2 salmonella
120	90.5	5.6	422	16	Q8Y778	Q8y778 listeria mo	193	86	5.3	338	12	Q91T16	Q91ti6 tubaia herp
121	90.5	5.6	446	10	Q7X605	Q7x605 oryza sativ	194	86	5.3	390	13	Q919U3	Q919u3 lagopus lag
122	90.5	5.6	485	11	Q9D5R5	Q9d5r5 mus musculu	195	86	5.3	496	1	Q34184	Q34184 halobacteri
123	90.5	5.6	2109	12	Q8BOH0	Q8boh0 vesicular s	196	86	5.3	532	2	Q9F7M5	Q9f7m5 gamma-prote
124	90.5	5.6	4876	5	Q8MUM9	Q8mum9 drosophila	197	85.5	5.3	419	10	Q9FQ10	Q9fq10 medicago tr
125	90.5	5.6	4904	5	Q9VH01	Q9vh01 drosophila	198	85.5	5.3	422	5	Q817J0	Q817j0 caenorhabdi
126	90	5.6	291	16	Q822S6	Q822s6 salmonella	199	85.5	5.3	442	11	Q8V187	Q8v187 mus musculu
127	90	5.6	373	2	Q69067	Q69067 pseudomonas	200	85.5	5.3	512	10	Q84QB2	Q84qb2 oryza sativ
128	90	5.6	399	17	Q8PWD2	Q8pwd2 methanosarc	201	85.5	5.3	516	5	Q21982	Q21982 caenorhabdi
129	90	5.6	596	11	Q8UZW8	Q8jzw9 mus musculu	202	85.5	5.3	685	16	Q88LT9	Q88lt9 pseudomonas
130	90	5.6	660	16	Q8ZP78	Q8zpw78 salmonella	203	85	5.3	247	16	Q8ZRH5	Q8zrh5 salmonella
131	89.5	5.5	258	16	Q83R03	Q83r03 s imidazole	204	85	5.3	378	16	Q9AAZ9	Q9aaz9 caulobacter
132	89.5	5.5	291	16	Q82DU8	Q82du8 listeria in	205	85	5.3	389	16	Q7W3T6	Q7w3t6 bordetella
133	89.5	5.5	291	16	Q8Y935	Q8y935 listeria mo	206	85	5.3	399	16	Q7W055	Q7w055 bordetella
134	89.5	5.5	294	16	Q8VJZ7	Q8vjz7 mycobacteri	207	85	5.3	509	16	Q81X77	Q81x77 bacillus an
135	89.5	5.5	300	16	Q61355	Q61355 mycobacteri	208	85	5.3	509	16	Q815K7	Q815k7 bacillus ce
136	89.5	5.5	300	16	Q7VEW2	Q7vew2 mycobacteri	209	85	5.3	511	16	Q921J2	Q921j2 rickettsia
137	89.5	5.5	324	16	Q83Z25	Q83z25 enterococcu	210	85	5.3	607	16	Q8DBM0	Q8dbm0 vibrio vuln
138	89.5	5.5	437	16	Q81Z78	Q81z78 bacillus an	211	85	5.3	906	16	Q9RTN7	Q9rtn7 deinococcus
139	89.5	5.5	499	16	Q8P7K2	Q8p7k2 xanthomonas	212	85	5.3	973	16	Q88M14	Q88m14 pseudomonas
140	89.5	5.5	527	16	Q83S32	Q83s32 ehigella fl	213	85	5.3	1012	16	Q7UHJ9	Q7uhj9 rhodospirell
141	89.5	5.5	548	2	Q9BM70	Q9bmj0 neisseria m	214	85	5.3	1723	4	Q9Y4F4	Q9y4f4 homo sapien
142	89.5	5.5	604	17	Q9YFCZ3	Q9ycz3 aeropyrum p	215	84.5	5.2	381	16	Q9X1R7	Q9x1r7 thermotoga
143	89.5	5.5	816	2	Q9AHT9	Q9ant9 streptococc	216	84.5	5.2	430	17	Q9YX55	Q9yex5 homo sapien
144	89.5	5.5	1339	3	Q8TFJ6	Q8tfj6 klebsiellomyc	217	84.5	5.2	480	17	Q9YU11	Q9yuy1 pyrococcus
145	89	5.5	481	10	Q81MP9	Q81mp9 oryza sativ	218	84.5	5.2	538	11	Q80XK0	Q80xk0 mus musculu
146	89	5.5	700	16	Q91338	Q91338 pseudomonas	219	84.5	5.2	545	16	Q9HVN7	Q9hvn7 pseudomonas
147	89	5.5	891	5	Q18602	Q18602 caenorhabdi	220	84.5	5.2	642	3	Q9JU76	Q9ju76 schizosacch
148	89	5.5	241	12	Q81HJ2	Q81hj2 avian param	221	84.5	5.2	875	2	Q9RAA4	Q9raa4 rickettsia
149	88.5	5.5	424	16	Q82UW8	Q82uw8 rhizobium m	222	84.5	5.2	944	12	Q9D9G6	Q9d9g6 rat cytomeg
150	88.5	5.5	437	16	Q8I1F1	Q8i1f1 bacillus ce	223	84.5	5.2	1789	5	Q8T145	Q8t145 dictyosteli
151	88.5	5.5	470	2	Q9X5S1	Q9x5s1 streptomyce	224	84	5.2	285	13	Q7S2Z9	Q7s2z9 xenopus lae
152	88.5	5.5	802	16	Q8LJRO	Q8ljro zea mays (m	225	84	5.2	374	16	P73953	P73953 synchocyst
153	88.5	5.5	802	16	Q97QW8	Q97qm8 streptococc	226	84	5.2	392	5	Q9W253	Q9w253 drosophila
154	88.5	5.5	828	16	Q8DPQ2	Q8dpq2 streptococc	227	84	5.2	426	16	Q8DB10	Q8db10 vibrio vuln
155	88	5.5	367	2	Q84DG7	Q84dg7 escherichia	228	84	5.2	437	10	Q9ASX8	Q9asx8 arabidopsis
156	88	5.4	416	16	Q93KZ1	Q93kz1 bradyrhizob	229	84	5.2	465	5	Q22129	Q22129 caenorhabdi
157	88	5.4	417	16	Q8FRV2	Q8frv2 corynebacte	230	84	5.2	576	2	Q60113	Q60113 zymomonas m
158	88	5.4	427	16	Q9K9G9	Q9k9g9 bacillus ha	231	84	5.2	585	12	Q07041	Q07041 variola vir
159	88	5.4	486	16	Q8FRP2	Q8fry2 corynebacte	232	84	5.2	592	10	Q9FHN6	Q9fhn6 arabidopsis
160	88	5.4	491	10	Q8LPV6	Q8lpv6 deschampsia	233	84	5.2	599	4	Q9H5P1	Q9h5p1 homo sapien
161	88	5.4	525	17	Q9T122	Q9t122 methanosarc	234	84	5.2	605	4	Q96MW7	Q96mw7 homo sapien
162	88	5.4	546	2	Q9KTX5	Q9ktx5 flavobacter	235	84	5.2	787	16	Q8F093	Q8f093 leptospira

236	84	5.2	1056	4	Q9H3R0	Q9h3r0 homo sapien	309	81.5	5.0	542	2	068872	068872 myxococcus
237	83.5	5.2	133	9	Q8SCV7	Q8scv7 pseudomonas	310	81.5	5.0	548	16	053560	053560 mycobacteri
238	83.5	5.2	347	10	Q93VR8	Q93vr8 arabidopsis	311	81.5	5.0	548	16	Q7TMB7	Q7tmb7 mycobacteri
239	83.5	5.2	349	5	O44538	O44538 caenorhabdi	312	81.5	5.0	570	10	Q9LU36	Q9lu36 arabidopsis
240	83.5	5.2	468	16	Q93IW3	Q93iw3 streptomyce	313	81.5	5.0	601	16	Q9I3W1	Q9i3w1 pseudomonas
241	83.5	5.2	482	16	Q8NUN8	Q8num8 staphylococ	314	81.5	5.0	607	10	Q91GSS	Q91gs5 oryza sativ
242	83.5	5.2	482	16	Q8NUN8	Q8num8 staphylococ	315	81.5	5.0	607	10	Q91GSS	Q91gs5 oryza sativ
243	83.5	5.2	519	16	Q8M5H8	Q83bh2 coxiella bu	316	81.5	5.0	694	10	Q7XWQ5	Q7xwq5 oryza sativ
244	83.5	5.2	595	10	Q8M5H8	Q8w5l8 oryza sativ	317	81.5	5.0	694	10	Q88VS3	Q88v83 lactobacill
245	83.5	5.2	595	10	Q7XHT2	Q7xh72 oryza sativ	318	81.5	5.0	898	10	Q8FVE9	Q8fve9 nicotiana t
246	83.5	5.2	726	16	Q8FKI8	Q8pk18 xanthomonas	319	81.5	5.0	902	2	084F16	Q84f16 clostridium
247	83.5	5.2	796	11	Q9IY06	Q9iy06 mus musculu	320	81.5	5.0	930	2	Q59290	Q59290 clostridium
248	83.5	5.2	861	16	Q88NQ1	Q88nq1 pseudomonas	321	81.5	5.0	940	16	Q9JTX2	Q9jtx2 neisseria m
249	83.5	5.2	1398	1	Q9P9L1	Q9p9l1 pyrococcus	322	81.5	5.0	965	2	Q9ZHV5	Q9zhv5 neisseria m
250	83.5	5.2	4074	4	Q86Z26	Q86z26 homo sapien	323	81.5	5.0	987	16	Q9RWP6	Q9rwp6 deinococcus
251	83	5.1	331	10	Q8LKN6	Q8lkn6 petunia hyb	324	81	5.0	1467	10	Q9M033	Q9m033 arabidopsis
252	83	5.1	390	5	Q8IA36	Q8ia36 drosophila	325	81	5.0	265	2	Q9F7R6	Q9f7r6 gamma-prote
253	83	5.1	400	16	Q99SH3	Q99sh3 staphylococ	326	81	5.0	265	10	Q8LQG9	Q8lqg9 oryza sativ
254	83	5.1	470	16	Q82VH7	Q82vh7 nitrosomona	327	81	5.0	332	12	Q9PYL8	Q9pyl8 xestia c-ni
255	83	5.1	472	16	Q92BX9	Q92bx9 listeria in	328	81	5.0	381	16	Q9WZ94	Q9wz94 thermotoga
256	83	5.1	472	16	Q9Y7B0	Q9y7b0 listeria mo	329	81	5.0	382	5	Q9VSS3	Q9vss3 drosophila
257	83	5.1	479	11	Q9QWV7	Q9qvw7 mus musculu	330	81	5.0	438	16	Q8FF63	Q8ff63 xanthomonas
258	83	5.1	518	10	Q9MBE5	Q9mbes lotus japon	331	81	5.0	503	5	Q9VAP6	Q9vap6 drosophila
259	83	5.1	818	11	Q9IY08	Q9iy08 mus musculu	332	81	5.0	629	16	Q92KY6	Q92ky6 rhizobium m
260	83	5.1	875	2	Q9RLA6	Q9rla6 rickettsia	333	81	5.0	653	5	Q95XJ5	Q95yj5 ciona intes
261	83	5.1	1021	10	Q7XKA2	Q7xka2 oryza sativ	334	81	5.0	858	5	Q9VGM0	Q9vgm0 drosophila
262	83	5.1	2096	16	Q7TWN7	Q7twn7 mycobacteri	335	81	5.0	908	17	Q8QOE6	Q8qoe6 methanosarc
263	83	5.1	3157	16	Q5O378	Q5o378 mycobacteri	336	81	5.0	1022	10	Q9LQK8	Q9lqk8 oryza sativ
264	82.5	5.1	343	17	Q97AH1	Q97ah1 thermoplasm	337	81	5.0	1234	5	Q7YXD0	Q7yxd0 caenorhabdi
265	82.5	5.1	422	16	Q92BT7	Q92bt7 listeria in	338	81	5.0	1520	5	Q7YSD0	Q7ysd0 caenorhabdi
266	82.5	5.1	511	16	Q9ZDL4	Q9zdl4 rickettsia	339	81	5.0	1549	5	Q8MM94	Q8mm94 caenorhabdi
267	82.5	5.1	562	16	P71654	P71654 mycobacteri	340	81	5.0	1583	5	Q8MLZ1	Q8mlz1 caenorhabdi
268	82.5	5.1	562	16	P71654	P71654 mycobacteri	341	81	5.0	1583	5	Q8MV03	Q8mv03 caenorhabdi
269	82.5	5.1	579	16	Q7TXU8	Q7txu8 mycobacteri	342	81	5.0	1654	5	Q7YSI9	Q7ysi9 caenorhabdi
270	82.5	5.1	601	16	Q835Z6	Q835z6 enterococcu	343	81	5.0	2078	5	P91834	P91834 caenorhabdi
271	82.5	5.1	875	2	Q9RLA9	Q9rla9 rickettsia	344	81	5.0	2847	4	Q15018	Q15018 homo sapien
272	82.5	5.1	888	10	Q9SIB9	Q9sib9 arabidopsis	345	80.5	5.0	234	10	Q94K08	Q94k08 arabidopsis
273	82.5	5.1	990	10	Q8L784	Q8l784 arabidopsis	346	80.5	5.0	281	16	Q92QG5	Q92qg5 rickettsia
274	82.5	5.1	2105	12	Q68772	Q68772 sinian hemo	347	80.5	5.0	282	16	Q8XZX2	Q8xxz2 rickettsia
275	82.5	5.1	2264	5	Q812E3	Q812e3 plasmodium	348	80.5	5.0	349	11	Q8OW86	Q8ow86 mus musculu
276	82	5.1	206	5	Q9N418	Q9n418 caenorhabdi	349	80.5	5.0	370	17	Q8OW86	Q8ow86 mus musculu
277	82	5.1	322	16	Q9PC38	Q9pc38 xylella fas	350	80.5	5.0	370	17	Q8OW86	Q8ow86 mus musculu
278	82	5.1	398	5	Q8MS90	Q8ms90 drosophila	351	80.5	5.0	395	16	Q9FTV4	Q9ftv4 deinoecoccus
279	82	5.1	505	4	Q8TBP8	Q8tbp8 homo sapien	352	80.5	5.0	416	10	Q9FTS2	Q9fts2 oryza sativ
280	82	5.1	511	13	Q7ZXP7	Q7zxp7 xenopus lae	353	80.5	5.0	416	10	Q9FTS2	Q9fts2 oryza sativ
281	82	5.1	526	16	Q8FTE3	Q8fte3 corynebacte	354	80.5	5.0	491	16	Q8YGA4	Q8yga4 brucella me
282	82	5.1	539	16	Q8NLL9	Q8nll9 corynebacte	355	80.5	5.0	516	6	Q8SQ69	Q8sq69 sus scrofa
283	82	5.1	543	16	Q9CM05	Q9cm05 pasteurella	356	80.5	5.0	521	5	Q8ISX7	Q8isx7 drosophila
284	82	5.1	548	11	Q8OTG4	Q8otg4 mus musculu	357	80.5	5.0	567	12	Q8VS26	Q8vs26 cochlitolobu
285	82	5.1	554	16	Q7WDJ5	Q7wdj5 bordetella	358	80.5	5.0	847	3	Q7Z8L6	Q7z8l6 lycopersico
286	82	5.1	554	16	Q7W2K1	Q7w2k1 bordetella	359	80.5	5.0	898	10	Q84TR4	Q84tr4 lycopersico
287	82	5.1	563	16	Q7VSD6	Q7vds6 bordetella	360	80.5	5.0	1040	16	Q89DV7	Q89dv7 bradyrhizob
288	82	5.1	602	11	Q8BWA1	Q8bwa1 mus musculu	361	80.5	5.0	1127	3	Q9P571	Q9p571 neurospora
289	82	5.1	632	2	Q7X517	Q7x517 campylobact	362	80.5	5.0	1307	11	Q8CJC2	Q8cjc2 mus musculu
290	82	5.1	658	11	Q8BUY6	Q8buy6 mus musculu	363	80.5	5.0	1741	5	O46095	O46095 drosophila
291	82	5.1	695	11	Q8OU56	Q8ou56 mus musculu	364	80.5	5.0	3432	12	Q90297	Q90297 japanes en
292	82	5.1	739	16	Q826H9	Q826h9 streptomyce	365	80.5	5.0	432	10	Q90297	Q90297 japanes en
293	82	5.1	869	16	Q8PME6	Q8pmf6 xanthomonas	366	80	4.9	201	10	Q9T0A4	Q9t0a4 arabidopsis
294	82	5.1	1054	11	Q8VCD7	Q8vcd7 mus musculu	367	80	4.9	250	10	Q9T0A4	Q9t0a4 arabidopsis
295	82	5.1	1098	4	Q9WTN8	Q9wtnd8 mus musculu	368	80	4.9	333	16	Q87746	Q87746 enterococcu
296	82	5.1	1100	4	Q94877	Q94877 homo sapien	369	80	4.9	373	2	Q9ZGC0	Q9zgc0 streptomyce
297	82	5.1	1392	12	Q9QTC5	Q9qtc5 marek's dis	370	80	4.9	397	17	Q9V808	Q9v808 aeropyrum p
298	82	5.1	1458	5	Q80895	Q80895 triphneustes	371	80	4.9	399	16	Q8A3I8	Q8a3i8 bacteroides
299	82	5.1	1991	2	Q83VG6	Q83vg6 erysipeloth	372	80	4.9	413	13	Q9I137	Q9i137 columba liv
300	81.5	5.0	240	16	Q815X3	Q815x3 bacillus ce	373	80	4.9	430	16	Q88GV4	Q88gv4 pseudomonas
301	81.5	5.0	331	16	Q8ZML1	Q8zml1 salmonella	374	80	4.9	430	16	Q7U3T1	Q7u3t1 synecococc
302	81.5	5.0	332	2	Q9ZAE0	Q9zae0 lactococcus	375	80	4.9	431	2	Q9RMU1	Q9rmu1 klebsiella
303	81.5	5.0	355	17	Q9ZAE0	Q9zae0 lactococcus	376	80	4.9	526	16	Q8ZQX2	Q8zqn2 salmonella
304	81.5	5.0	394	9	Q8SAP9	Q8spw9 methanosarc	377	80	4.9	535	11	Q8OUW0	Q8ouw0 mus musculu
305	81.5	5.0	395	2	Q8SD91	Q8sd91 pseudomonas	378	80	4.9	548	17	Q8TR30	Q8tr30 methanosarc
306	81.5	5.0	511	11	Q9WTV7	Q9wuv7 rattus norv	379	80	4.9	869	10	Q94GG1	Q94gg1 oryza sativ
307	81.5	5.0	519	11	Q91VZ1	Q91vz1 mus musculu	380	80	4.9	981	16	Q89S67	Q89s67 bradyrhizob
308	81.5	5.0	525	16	Q9JXJ7	Q9jxj7 neisseria m	381	80	4.9	1008	5	Q8NR76	Q8nr76 drosophila

382	80	4.9	1346	3	Q871M6	Q871m6 neurospora	455	78.5	4.9	368	10	Q9LSR0	Q9lsr0 arabidopsis
383	80	4.9	1384	16	Q7USX6	Q7usx6 rhodospirillum rubrum	456	78.5	4.9	374	17	Q8TXL3	Q8txl3 methanopyrus
384	80	4.9	1813	10	Q92SC9	Q92sc9 lactuca sativa	457	78.5	4.9	387	2	Q32633	Q32633 helicobacter
385	80	4.9	2268	5	Q81AN5	Q81an5 plasmodium falciparum	458	78.5	4.9	427	2	Q9S1L6	Q9s1l6 streptococcus
386	80	4.9	2799	4	Q81ZF6	Q81zf6 homo sapien	459	78.5	4.9	441	10	Q84LL3	Q84ll3 zea mays su
387	79.5	4.9	274	2	Q87874	Q87874 bordetella pertussis	460	78.5	4.9	477	2	Q8L2C3	Q8l2c3 proteus vul
388	79.5	4.9	276	16	Q89RTL4	Q89rtl4 deinococcus	461	78.5	4.9	479	16	Q82TM7	Q82tm7 streptomycete
389	79.5	4.9	311	4	Q81VJ4	Q81vj4 homo sapien	462	78.5	4.9	481	16	Q7UVW77	Q7uvw77 rhodospirillum rubrum
390	79.5	4.9	312	16	Q7W267	Q7w267 bordetella pertussis	463	78.5	4.9	523	16	Q9ZN39	Q9zn39 helicobacter
391	79.5	4.9	333	2	Q83007	Q83007 aeromonas p	464	78.5	4.9	529	16	Q92JT2	Q92jt2 rhizobium m
392	79.5	4.9	364	2	Q81CB3	Q81cb3 streptomycete	465	78.5	4.9	534	10	Q9FNI7	Q9fni7 arabidopsis
393	79.5	4.9	367	5	Q7YUQ8	Q7yqu8 trypanosoma	466	78.5	4.9	545	5	Q27620	Q27620 drosophila
394	79.5	4.9	379	2	Q8KXV8	Q8kxv8 shigella boydii	467	78.5	4.9	550	11	Q8VC10	Q8vc10 mus musculus
395	79.5	4.9	386	16	Q89EF9	Q89ef9 bradyrhizobium	468	78.5	4.9	550	11	Q9DLS0	Q9dlis0 mus musculus
396	79.5	4.9	397	16	Q50518	Q50518 streptomycete	469	78.5	4.9	559	10	Q7XJE8	Q7xje8 prunus dulcis
397	79.5	4.9	416	16	Q7YIS5	Q7yis5 clostridium	470	78.5	4.9	604	17	Q9VON3	Q9von3 pyrococcus
398	79.5	4.9	425	16	Q7V9T2	Q7v9t2 prochlorococcus	471	78.5	4.9	608	16	Q8ZND9	Q8znd9 salmonella
399	79.5	4.9	445	4	Q96M27	Q96m27 homo sapien	472	78.5	4.9	608	16	Q82523	Q82523 salmonella
400	79.5	4.9	462	4	Q81VL4	Q81vl4 homo sapien	473	78.5	4.9	656	11	Q8CEI8	Q8cei8 mus musculus
401	79.5	4.9	484	4	Q86Y42	Q86y42 homo sapien	474	78.5	4.9	660	16	Q8B8N4	Q8b8n4 shewanella
402	79.5	4.9	484	16	Q8G729	Q8g729 bifidobacterium	475	78.5	4.9	665	16	Q97K46	Q97k46 clostridium
403	79.5	4.9	545	17	Q98OU2	Q98ou2 sulfobacillus	476	78.5	4.9	674	16	Q9KXQ3	Q9kxq3 bacillus ha
404	79.5	4.9	548	2	Q9RMJ3	Q9rmj3 neisseria g	477	78.5	4.9	691	5	Q95Z95	Q95z95 leishmania
405	79.5	4.9	570	10	Q84P22	Q84p22 arabidopsis	478	78.5	4.9	715	10	Q9FYT6	Q9fyt6 zea mays m
406	79.5	4.9	604	2	Q9Z187	Q9z187 bacillus st	479	78.5	4.9	776	16	Q8QI18	Q8qi18 bradyrhizob
407	79.5	4.9	783	11	Q8S883	Q8s883 mus musculus	480	78.5	4.9	804	10	Q9SHM4	Q9shm4 arabidopsis
408	79.5	4.9	788	5	Q9VGL9	Q9vgl9 drosophila	481	78.5	4.9	848	16	Q9CHQ5	Q9chq5 lactococcus
409	79.5	4.9	805	11	Q8C842	Q8c842 mus musculus	482	78.5	4.9	890	10	Q9LJ50	Q9lj50 arabidopsis
410	79.5	4.9	877	16	Q8XSY7	Q8xsy7 ralstonia s	483	78.5	4.9	909	16	Q8R6Z3	Q8r6z3 thermoplasma
411	79.5	4.9	898	10	Q8ANI5	Q8ani5 lycopersicon	484	78.5	4.9	917	5	Q8T9A1	Q8t9a1 drosophila
412	79.5	4.9	911	4	Q81V66	Q81v66 homo sapien	485	78.5	4.9	1005	11	Q8BLR5	Q8blr5 mus musculus
413	79.5	4.9	986	10	Q93416	Q93416 oryza sativ	486	78.5	4.9	1312	3	Q8WV2	Q8wv2 neurospora
414	79.5	4.9	988	10	Q64454	Q64454 oryza sativ	487	78.5	4.9	1654	16	Q8YV86	Q8yv86 anabaena sp
415	79.5	4.9	1072	16	Q9CF64	Q9cf64 lactococcus	488	78.5	4.9	2124	16	Q9SM03	Q9sm03 rhizobium l
416	79.5	4.9	1179	4	Q60271	Q60271 homo sapien	489	78.5	4.9	3424	5	Q9VT22	Q9vt22 drosophila
417	79.5	4.9	1204	15	Q7KZ29	Q7kz29 recombinant	490	78.5	4.9	3479	5	Q9GFT8	Q9gft8 drosophila
418	79.5	4.9	1257	10	Q64516	Q64516 arabidopsis	491	78.5	4.9	3479	5	Q9VT28	Q9vt28 drosophila
419	79.5	4.9	1311	4	Q81ZX7	Q81zx7 homo sapien	492	78	4.8	115	11	Q80VM6	Q80vm6 mus musculus
420	79.5	4.9	1506	5	Q7YU30	Q7yu30 drosophila	493	78	4.8	173	11	Q99M72	Q99m72 mus musculus
421	79.5	4.9	1520	5	Q8B863	Q8b863 drosophila	494	78	4.8	242	16	Q8Y8M0	Q8y8m0 listeria mo
422	79.5	4.9	2535	10	Q81018	Q81018 arabidopsis	495	78	4.8	293	16	Q7TVE2	Q7tve2 mycobacteri
423	79	4.9	247	16	Q8Z922	Q8z922 salmonella	496	78	4.8	293	17	Q82WL6	Q82wl6 pyrobaculum
424	79	4.9	354	2	Q8KQ27	Q8kq27 streptomycete	497	78	4.8	304	13	Q7ZYH0	Q7zyh0 xenopus lae
425	79	4.9	372	10	Q80512	Q80512 arabidopsis	498	78	4.8	313	16	Q7V0G9	Q7v0g9 prochlorococcus
426	79	4.9	410	16	Q05446	Q05446 mycobacteri	499	78	4.8	328	16	Q9KYM8	Q9kym8 streptomycete
427	79	4.9	451	13	Q7ZTV9	Q7ztv9 brachydanio	500	78	4.8	336	17	Q9HPL0	Q9hpl0 halobacteri
428	79	4.9	504	16	Q89XV7	Q89xv7 bradyrhizob							
429	79	4.9	506	13	Q9PVI1	Q9pvi1 fundulus he							
430	79	4.9	514	2	Q8KYZ3	Q8kyz3 uncultured							
431	79	4.9	531	5	Q8T8Q4	Q8t8q4 drosophila							
432	79	4.9	540	10	Q9PL17	Q9pl17 arabidopsis							
433	79	4.9	562	16	Q8BKJ7	Q8bkj7 pseudomonas							
434	79	4.9	571	16	Q8KBC7	Q8kbc7 chlorobium							
435	79	4.9	588	2	Q63007	Q63007 thermus sp.							
436	79	4.9	610	17	Q97V19	Q97v19 sulfobacillus							
437	79	4.9	632	17	Q929794	Q929794 archaeoglobus							
438	79	4.9	720	10	Q941N7	Q941n7 phytophthor							
439	79	4.9	758	16	Q7UYU1	Q7uyy1 rhodospirillum rubrum							
440	79	4.9	900	10	Q93VK2	Q93vk2 phytophthor							
441	79	4.9	900	10	Q941N6	Q941n6 phytophthor							
442	79	4.9	907	10	Q9S236	Q9s236 arabidopsis							
443	79	4.9	995	10	Q94A28	Q94a28 xanthomonas							
444	79	4.9	1090	16	Q9P6S5	Q9p6s5 xanthomonas							
445	79	4.9	1207	11	Q8BKJ1	Q8bkj1 mus musculus							
446	79	4.9	1207	11	Q8BJE0	Q8bje0 mus musculus							
447	79	4.9	1279	10	Q8SA93	Q8sa93 zea mays m							
448	78.5	4.9	224	10	Q84LL2	Q84ll2 zea mays su							
449	78.5	4.9	270	16	Q8RGJ9	Q8rgj9 fusobacteri							
450	78.5	4.9	293	16	Q8NY90	Q8ny90 staphylococcus							
451	78.5	4.9	314	16	Q07521	Q07521 bacillus su							
452	78.5	4.9	342	16	Q7UVH8	Q7uvh8 rhodospirillum rubrum							
453	78.5	4.9	355	3	Q7ZA39	Q7za39 emericella							
454	78.5	4.9	361	17	Q974W0	Q974w0 sulfobacillus							

ALIGNMENTS

RESULT 1

Q8NCC9 PRELIMINARY; PRT; 975 AA.

AC Q8NCC9, Q8NCC9, 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE Hypothetical protein FLJ90334.

OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CX NCBI_TaxID=9606;
 [1]

SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
 RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
 FT "NEDO human cDNA sequencing project."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK074875; BAC11227.1; -.

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KW Hypothetical protein.
SQ SEQUENCE 975 AA; 107283 MW; 35B24685674A9B35 CRC64;

Query Match 100.0%; Score 1617; DB 4; Length 975;
Best Local Similarity 100.0%; Pred. No. 1.5e-136; Mismatches 0; Indels 0; Gaps 0;
Matches 310; Conservative 0;

QY 1 MRLGSGTPTCCVAIEVLGIAVFLRGGFPAPVRSSARAEGHGAEPFPAPEPSAGASSNWTTL 60
DB 1 MRLGSGTPTCCVAIEVLGIAVFLRGGFPAPVRSSARAEGHGAEPFPAPEPSAGASSNWTTL 60
QY 61 PPLPSKVVIVLIDALRDDVFSGKGVKMPMTTTLVEKGASHSVAAEKPTVTMPRIK 120
DB 61 PPLPSKVVIVLIDALRDDVFSGKGVKMPMTTTLVEKGASHSVAAEKPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLESVIRQAAGKRIIVFYGDETWVKLFPKHFEYDGT 180
DB 121 ALMTGSLPGFVDVIRNLNSPALLESVIRQAAGKRIIVFYGDETWVKLFPKHFEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDMDILILHYLGLDHIHISGPNPLIGQKLSMD 240
DB 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDMDILILHYLGLDHIHISGPNPLIGQKLSMD 240
QY 241 SVLMKHTLSQSKERTPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
DB 241 SVLMKHTLSQSKERTPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
DB 301 GDIRHPKHVQ 310

RESULT 2
Q8N866 PRELIMINARY; PRT; 299 AA.
AC Q8N866;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Hypothetical protein FLJ39925.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
RA Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,
RA Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK097244; BAC04984.1; -.
KW Hypothetical protein.
SQ SEQUENCE 299 AA; 32913 MW; 73D96DBS3EAL1006 CRC64;

Query Match 71.5%; Score 1156; DB 4; Length 299;
Best Local Similarity 100.0%; Pred. No. 9.6e-96;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 MPYTYLVEKGASHSVAAEKPTVTMPRIKALMTGSLPGFVDVIRNLNSPALLESVIR 149
DB 1 MPYTYLVEKGASHSVAAEKPTVTMPRIKALMTGSLPGFVDVIRNLNSPALLESVIR 60
QY 150 QAKAAGKRIIVFYGDETWVKLFPKHFEYDGTTSFFVSDYTEVDNNVTRHLDKVLKRGDMD 209
DB 61 QAKAAGKRIIVFYGDETWVKLFPKHFEYDGTTSFFVSDYTEVDNNVTRHLDKVLKRGDMD 120
QY 210 ILILHYLGLDHIHISGPNPLIGQKLSMDSVLMKHTLSQSKERTPLNLLVLCGDH 269
DB 121 ILILHYLGLDHIHISGPNPLIGQKLSMDSVLMKHTLSQSKERTPLNLLVLCGDH 180
QY 270 GMSGTGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ 310
DB 181 GMSGTGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ 221

RESULT 4
Q86ITS PRELIMINARY; PRT; 1734 AA.
AC Q86ITS;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to 40 kDa putative membrane-spanning Atgase; Mspip.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
CX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer A., Rosenthal A., Nogel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
```



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Query Match 36.5%; Score 590; DB 10; Length 897;
Best Local Similarity 40.6%; Pred. No. 5e-44;
Matches 119; Conservative 56; Mismatches 108; Indels 10; Gaps 3;

QY 8 FATCCVAIEVLGIAVFLRGPPA-PVRSARAEGHGAEPAPPEPAGASSNWTTLPPPLFS 66
DB 14 FVAGILQIGLSIFVGFPPVKETLGVSGSEYRDFCDSS--LISNESELHHPEKL 71
QY 67 KVVIVLIDALRDDVFVSGK-----VKFMPYTYLVKEGASHSFVAEAKPPTVTPRI 119
DB 72 RLLYQVIDGLPAEFVLGDKGPEKVKLESMPYTSLLANGDAIGYHAKAAPPTVTPRL 131
QY 120 KALMTGSLPGFVDVNRNLNSPALLEDVIRQAKAGKIVFGDGTWVKLPKHFVEVDG 179
DB 132 KAWVSGAIGGFLDVAFNFTQALLDDNLGQFRIGWKVMMLGDETLWKLPGFLFMRHDG 191
QY 180 TTSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHGHSNPSPLIGOKLSEM 239
DB 192 VSSFFVKDVQVDRVNRHLPDELNSDDWNLILHYLGLDGHGHSNPSPLMPAKLXEM 251
QY 240 DSVLMKIHTSLOSKERETPLNLLVLCGDHGMSETSGHSGASSTEVEVNTPLILI 292
DB 252 DDIVRTMHLAMDRSHDQQTLLIIVSDHGMTEGNHGGSSYEETSLMLFI 304

RESULT 7
Q8TGB2 PRELIMINARY; PRT; 892 AA.
AC Q8TGB2;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Putative Gpi7p.
GN GPI7.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC5314;
RA Richard M., Ibat-Ombetta S., Dromer F., Bordon-Pallier F.,
RA Jouault T., Gaillardin C.;
RT "Complete Glycosylphosphatidylinositol Anchors are Required in Candida
RT albicans for Full Morphogenesis, Virulence and Resistance to
RT Macrophages.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF348498; AAL83897.1; .
SQ SEQUENCE 892 AA; 101554 MW; BF04A57E0356C247 CRC64;

Query Match 36.1%; Score 583; DB 3; Length 892;
Best Local Similarity 42.6%; Pred. No. 2.1e-43;
Matches 127; Conservative 46; Mismatches 91; Indels 34; Gaps 8;

QY 15 IEVLGTAFLRGPPAPVRSARAEGHGAEPAPPEPAGASSNWTTLP-----PPLFSKV 68
DB 18 INIIGFLVFLRGPPFSKV-----VLPGFNFGDSTKSPFDHGTPOFNF 63
QY 69 VIVLIDALRDDVFVSGKGVKMPYTYLVKEGASHSFVAEAKPPTVTPRIKALMTGSLP 128
DB 64 ILMVVDNRSDFCFSR--SNFSFLHQLNQGHALPPTAFSNPPTVTLPRKLGITGGTP 121
QY 129 GFVDVIRNL-----NSPAL-LEDSVIRQAK-AAGKRIVFGDGTWVKLPKHFVEVDGTT 181
DB 122 NFLDAILNAVDDQDSDQLGNQDSVHWQFRHSNNKTINFFGDDTLWKLFDQDQTEFEGTN 181
QY 182 SFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHGHSNPSPLIGOKLSEMS 241
DB 182 SFFVSDYTEVDNNVTRHLDQLSNKKWDGILILHYLGLDGHGHSNPSPLIGOKLSEMS 241
QY 242 VLMKIHTSLOSKERETPLNLLVLCGDHGMSETSGHSGASSTEVEVNTPLILISAFERK 299
DB 242 ILQRLYTVV-TKNDT----LIVLMGDHGMNEIGNHGGSSPGETSAALSIFSPKFNHK 294
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Query Match 32.4%; Score 524; DB 5; Length 795;
Best Local Similarity 42.4%; Pred. No. 3.7e-38;
Matches 108; Conservative 51; Mismatches 80; Indels 16; Gaps 5;

QY 67 KVVIVLIDALRDDVFVSGKGVKMPYTYLVKEGASHSFVAEAKPPTVTPRIKALMTGS 126
DB 104 RLVEFWVIDAFRLSFLTSGKSP--MSFTKSEITKSAKLFDAAYARMPVTLLPRITAYLTGT 161
QY 127 LPGFVDVIRNLNSPALLEDVIRQAKAGKRIVFGDGTWVKLPKHFVEVDGTTSPFVS 186
DB 162 LPSTGTLNLATAEMKTANNWISRIQIKGRKVFHFGDDTWIRLLPRSEFEKGVTSFVS 221
QY 187 DYTEVDNNVTRHLDKVLKRGD--WDILILHYLGLDGHGHSNPSPLIGOKLSEMSVLM 244
DB 222 DYTEVDNNVTRHLDTELSTNTHNSDALILHYLGLDGHGHSNPSPLIGOKLSEMSVLM 281
QY 245 KIHTSLOSKERETPLNLLVLCGDHGMSETSGHSGASSTEVEVNTPLILISAFERKPGD-- 302
DB 282 RIHKYLSK-SVTSVQESYLIIVCGDHGTAAGSHGASPDETRVPVPIWK--FGREGNKN 338
QY 303 -----LRHPKHVQ 310
DB 339 YGNQDLSLKQPPRIE 353

RESULT 9
Q9V4N0 PRELIMINARY; PRT; 927 AA.
AC Q9V4N0;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE CG2144 protein.
GN CG2144.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
```

OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scher S.E., Richards S., Ashburner M., Henderson S.N.,
 RA George R.A., Lewis S.E., Scher S.E., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Franckoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimbel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celnik S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Ananides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dreanek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragov V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Swirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celnik S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.

RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003840; AAF59237.3; -
 DR FlyBase; FBgn0033187; CG2144.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008233; P:peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000508; Peptidase_S26.
 DR PROSITE; PS00761; SPASE I_3; 1.
 SQ SEQUENCE 927 AA; 104588 MW; 1A543894BBAD7EF5 CRC64;
 Query Match 31.6%; Score 511.5; DB 5; Length 927;
 Best Local Similarity 41.1%; Pred. No. 6.2e-37;
 Matches 118; Conservative 43; Mismatches 99; Indels 27; Gaps 9;
 QY 19 GIAVFLRGFPFAPVRSSARAEHGAEPAPPEPSAGASSNMTLPPPLFSKVIVLIDALRD 78
 DB 21 GAVLFLGIFPPA---SYSAEKESTVPEGRPTALLGMLTP-PPAYDSFVLLVLDALRD 76
 QY 79 DFVFGSGVEMPYT-TYLVEKGAHSFVAEAKPPTVTPRIKALMTGSLPGVDVIRNL 137
 DB 77 DFDPATS---MPVAVSRACEKLEKLVHDI-----PTVTPLKSIITGTLNFDIALNV 127
 QY 138 NSPALLEDVIRQAKAGKRVFVGDVETVVKLPKPFHFV-EYDGTTSFFVSDYTEVDNNVT 196
 DB 128 GHTEQMQDSFLRLKQNRVVSFAGDHTVVKLPFSEFTRQVENHDSFYVNDFFEGDENV 187
 QY 197 RHLDKVLRGWDILILHYGLDHIHISGPNPLIGKQKLSMDSVLMKI--HTSLQSK 254
 DB 188 KLTETELEDSDWSILLIHLGLDHIHISGPNPLIGKQKLSMDSVLMKI--HTSLQSK 242
 QY 255 REPLPPLN-LIIVLCGDHGMSTGSHGASSTEVNTPPLILISSAFERKP 300
 DB 243 ----FFNVLLMLTGDRGVADGGHGGTNPATLIVPLIYLYNNCKTP 285
 RESULT 10
 Q9GM09 PRELIMINARY; PRT; 333 AA.
 ID Q9GM09 PRELIMINARY; PRT; 333 AA.
 AC Q9GM09, 2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OC NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB050262; BAB17014.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 333 AA; 37237 MW; 1D2EB0458ACCE97C CRC64;
 Query Match 31.6%; Score 511; DB 6; Length 333;
 Best Local Similarity 97.0%; Pred. No. 1.5e-37;
 Matches 98; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 210 ILIHLVGLDHIHISGPNPLIGKQKLSMDSVLMKIHTSLQSKRETPLNLLVLCGDH 269
 DB 1 MLILHLVGLDHIHISGPNPLIGKQKLSMDSVLMKIHTSLQSKRETPLNLLVLCGDH 60

DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
OS	Genomic DNA, chromosome 5, Pl clone:MKP11.
OS	Arabidopsis thaliana (Mouse-ear cress).
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi.
OX	NCBI_TaxID=3702;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Columbia;
RX	MEDLINE=97471969; PubMed=9330910;
RA	Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA	Miyajima N., Tabata S.
RT	"Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT	features of the 1.6 Mb regions covered by twenty physically assigned
RT	Pl clones."
RL	DNA Res. 4:215-230(1997).
DR	EMBL; AB005238; BAB10512.1; --
SQ	SEQUENCE 884 AA; 97926 MW; OE247D729AC6B30A CRC64;
Query Match	25.7%; Score 415.5; DB 10; Length 884;
Best Local Similarity	33.9%; Pred. No. 2.6e-28;
Matches 97; Conservative 46; Mismatches 114; Indels 29; Gaps 5;	
QY	15 IEVLGIATVLRGPF-----PAPVRSARAEHGAEPAPESAGASSNWTLPPLFLGKQVI 70
DB	18 IHAIALIITRGELLTRTELPHSTC-SDVLSLPCLASPSNHDS--SSEPKPMWKLTI 74
QY	71 VLIDALRDDVFSGKGVKMPYTYTILVEKGASHSFVAEAKPPTVTWPRIKALMTGSLPGF 130
DB	75 LOTLAFAND-----SSAKIFKAFADPPTTSLQRLKGLTTGGLPTF 114
QY	131 VDVIRNLSPALLEDSVIRQAAAGRIYVYGDETWVKLFPKHFEVDGTTSFVSDYTE 190
DB	115 IDIGNSFGAPAVEDNFINQLVNLGRVYMGDDTWTQFPNQFQKSPFPSPFNVDLDT 174
QY	191 VDNVNVTRHLDKVLKRGDWILILHYLGLDHIHISGFNSPLIGQKLSMDSVLMKIHTSL 250
DB	175 VDNGCIEHLFPTLFKDDVDVLAHFLGVDPHAGHIFGVDSSPMINKLEQYNSVLEKVINIL 234
QY	251 QSKERTPL--PNLLVLCGDHGMSETGSGASSTEWTPTLIISS 294
DB	235 ESQAGCGGLHENTMLIVMGDHGQTGLNGDHGGTAEEVETTFAMST 280
RESULT 15	
OL3663	PRELIMINARY; PRT; 918 AA.
ID	OL3663;
AC	OL3663;
DT	01-JAN-1998 (TrEMBLrel. 05, Created)
DT	01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	ORF YL031C.
GN	PI072 OR SPBC27B12.06.
OS	Schizosaccharomyces pombe (Fission yeast).
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;
OC	Schizosaccharomycetes.
OX	NCBI_TaxID=4896;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=972 H-;
RA	Kushida N., Yamazaki S., Tanaka T., Jinno K., Haikawa Y., Yamazaki J.,
RA	Yamamoto S., Sekine M., Oguchi A., Nagai Y., Sakai M., Aoki K.,
RA	Ogura K., Otsuka R., Kudoh Y., Yanagida M., Machida M., Zhang M.Q.;
RA	Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=972H-;
RA	Wood V., Rajandream M.A., Barrall B.G., Lauber J., Hilbert H.,
RA	Duesterhoeft A.;
RL	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AB004539; BAA21454.1; --

Search completed: August 2, 2004, 16:29:56
Job time : 53 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 2, 2004, 16:25:48 ; Search time 13 Seconds

(without alignments)
1241.673 Million cell updates/sec

Title: US-10-036-150-45

Perfect score: 1617

Sequence: 1 MRLGSGTFATCCVAIEVLGI.....LISSAFERKPGDIRHPKHVQ 310

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141691 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	634.5	39.2	758	1 YA93 SCHPO	Q09782 schizosacch
2	508.5	31.4	830	1 YJG2 YEAST	P40367 saccharomyc
3	490	30.3	1093	1 PIGO MOUSE	Q9j116 mus musculu
4	481	29.7	1088	1 PIGO HUMAN	Q8tq98 homo sapien
5	170	10.5	919	1 YKQ5 YEAST	P36051 saccharomyc
6	114	7.1	963	1 IRE2 RAT	Q62751 rattus norv
7	111.5	6.9	906	1 NPPI MOUSE	P06902 m ectionucle
8	111	6.9	885	1 NPPI RAT	Q64610 r ectionucle
9	109	6.7	589	1 SKS1 ARATH	Q8vxx5 arabidopsis
10	108.5	6.7	906	1 NPPI HUMAN	Q924c3 r ectionucle
11	107	6.6	875	1 NPP2 HUMAN	O14638 h ectionucle
12	105.5	6.5	863	1 NPP2 MOUSE	Q9rie6 m ectionucle
13	101.5	6.3	862	1 NPP1 HUMAN	P22413 h ectionucle
14	101	6.2	925	1 NPPI MYCPE	Q8ew33 mycoplasma
15	98.5	6.1	502	1 YCR6 YEAST	P23533 saccharomyc
16	97.5	6.0	742	1 YCR6 YEAST	P03523 vesicular s
17	96.5	6.0	2109	1 RRPL VSVSJ	P48455 mus musculu
18	95.5	5.9	513	1 P2BC MOUSE	Q9y5f3 homo sapien
19	95	5.9	818	1 CDB1 HUMAN	Q9v198 pyrococcus
20	94.5	5.8	388	1 TRB1 PYRAB	Q8u093 pyrococcus
21	94	5.8	388	1 TRB1 PYRFU	P16882 mus musculu
22	92.5	5.7	650	1 GHR MOUSE	P16310 rattus norv
23	92	5.7	638	1 GHR RAT	P48200 homo sapien
24	90.5	5.6	963	1 IRE2 HUMAN	Q28575 ovis aries
25	90	5.6	634	1 GHR SHEEP	Q43989 acinetobact
26	89.5	5.5	465	1 COBQ ACICA	Q06464 antithamilo
27	89.5	5.5	510	1 GPMI ANTSP	P12887 saccharomyc
28	89	5.5	359	1 UNG YEAST	Q8fg48 escherichia
29	88.5	5.5	258	1 HIS6 ECOL6	P10373 escherichia
30	88.5	5.5	258	1 HIS6 ECOLI	Q9d228 mus musculu
31	88.5	5.5	642	1 KF12 MOUSE	Q8t122 methanosarc
32	88	5.4	525	1 Y3J7 METAC	P97675 r ectionucle
33	88	5.4	875	1 NPP3 RAT	

34	87.5	5.4	1216	1 PIB1 BOVIN	P10894 bos taurus
35	87	5.4	311	1 LUCI RENEE	P27652 renilla ren
36	87	5.4	506	1 SYG DEIRA	Q958r5 deinococcus
37	86.5	5.3	365	1 C713 SOLME	P37119 solanum mel
38	86.5	5.3	477	1 MYPH HUMAN	Q43203 homo sapien
39	86.5	5.3	519	1 YA05 HAEIN	P44974 haemophilus
40	86.5	5.3	527	1 YBIP ECOLI	P75785 escherichia
41	86	5.3	485	1 Y740 HAEIN	Q57290 haemophilus
42	86	5.3	637	1 DNAK PSEAE	Q9hv43 pseudomonas
43	86	5.3	3396	1 PSCV HUMAN	P13611 homo sapien
44	85.5	5.3	389	1 TRPB PYRKO	Q9y9d0 pyrococcus
45	85.5	5.3	1216	1 PIB1 HUMAN	Q9nq66 homo sapien
46	85	5.3	431	1 HISX VIBPA	Q87q11 vibrio para
47	85	5.3	509	1 GPMI BACCA	Q81x77 bacillus an
48	85	5.3	509	1 GPMI BACCR	Q815k7 bacillus ce
49	85	5.3	510	1 GPMI LISIN	Q928i2 listeria in
50	85	5.3	510	1 GPMI LISMO	Q8y4i4 listeria mo
51	85	5.3	638	1 GHR MACMU	P79194 macaca mula
52	85	5.3	641	1 DNAK PSEPK	Q88du2 pseudomonas
53	85	5.3	1098	1 TSL1 YEAST	P38427 saccharomyc
54	84.5	5.2	258	1 HIS6 BUCAP	Q9zhe1 buchnera ap
55	84.5	5.2	810	1 SYFB SYN3	P74296 synecocyst
56	84	5.2	416	1 ALAT SHEEP	P12725 ovis aries
57	84	5.2	586	1 SYN2 RAT	Q63537 rattus norv
58	84	5.2	602	1 IF2P SULFO	Q976al sulfobolus
59	83.5	5.2	347	1 CACR ARATH	P27140 arabidopsis
60	83.5	5.2	403	1 TRB1 METAC	Q8tlp3 methanosarc
61	83.5	5.2	547	1 ESTA DROPS	P25727 drosophila
62	83.5	5.2	1398	1 PLS PYRFU	P72186 pyrococcus
63	83.5	5.2	4074	1 PKHD HUMAN	Q8tcz9 homo sapien
64	83	5.1	331	1 CACX FLABI	P45510 flaveria bi
65	83	5.1	357	1 Y21C MYCPN	P75470 mycoplasma
66	83	5.1	693	1 SYGB BACHD	Q9kd48 bacillus ha
67	83	5.1	2175	1 HMCU DROME	P10180 drosophila
68	82.5	5.1	368	1 ALR LISMO	Q85045 listeria mo
69	82.5	5.1	545	1 ESTB DROPE	O16172 drosophila
70	82.5	5.1	898	1 ACOC CUCMA	P49608 cucurbita m
71	82.5	5.1	986	1 RHG6 MOUSE	O54834 mus musculu
72	82	5.1	563	1 OXAA BORPA	Q7wzkl bordetella
73	82	5.1	563	1 OXAA BORPE	Q7vwd6 bordetella
74	82	5.1	767	1 TLE2 MOUSE	Q9wvb2 mus musculu
75	82	5.1	1986	1 WA EMENI	Q03149 emerisella
76	81.5	5.0	352	1 TRPD NEIMA	Q91gm3 neisseria m
77	81.5	5.0	420	1 RBL PYRFU	Q9ulp9 pyrococcus
78	81.5	5.0	519	1 SNK2 MOUSE	Q9cw8 mus musculu
79	81.5	5.0	521	1 P2BA MOUSE	P20652 mus musculu
80	81.5	5.0	694	1 SYGB LACPL	Q88vs3 lactobacill
81	81.5	5.0	795	1 LON MYCPN	P78025 mycoplasma
82	81.5	5.0	1234	1 RPOB CLOPE	Q93r88 clostridium
83	81	5.0	490	1 SYE BORBU	O51345 borrelia bu
84	81	5.0	512	1 GPMI OCEIH	P59174 oceanobacil
85	81	5.0	585	1 YEJM HAEIN	P44898 haemophilus
86	81	5.0	626	1 ILVB CORGL	P42463 corynebacte
87	81	5.0	656	1 DNK COXBU	O87712 coxiella bu
88	81	5.0	902	1 FTDH HUMAN	Q75891 homo sapien
89	81	5.0	921	1 DPOL RICHE	Q9rlb6 rickettsia
90	80.5	5.0	258	1 HIS6 SALTU	P10374 salmonella
91	80.5	5.0	505	1 GPMI MYCUP	Q98qa7 mycoplasma
92	80.5	5.0	537	1 SYR MYCGB	P47618 mycoplasma
93	80.5	5.0	751	1 GCP2 CAERL	P91406 caenorhabdi
94	80.5	5.0	1036	1 AXOI CHICK	P28685 gallus gall
95	80	4.9	391	1 HIS8 META	Q8tv93 methanopyru
96	80	4.9	424	1 PYRC STAAM	Q99ur7 staphylococ
97	80	4.9	440	1 GAT4 MOUSE	Q08369 mus musculu
98	80	4.9	638	1 DNAK PSESM	Q87wp0 pseudomonas
99	80	4.9	986	1 RECL DROME	P35600 drosophila
100	79.5	4.9	270	1 PYRD THEMA	Q9wyg8 thermotoga
101	79.5	4.9	548	1 ESTA DROPE	O16173 drosophila
102	79.5	4.9	560	1 SYR METH	O27496 methanobact
103	79.5	4.9	743	1 TLE2 HUMAN	Q40725 homo sapien
104	79.5	4.9	844	1 DNL4 HUMAN	P49917 homo sapien
105	79.5	4.9	1090	1 NIT4 NEUCR	P28349 neuropsora
106	79.5	4.9	1571	1 CS3_DROME	O77086 drosophila

107	79	4.9	368	1	ALR_LISIN	Q92dc9	listeria in	180	76	4.7	470	1	FUCK_HAEIN	P43399	haemophilus
108	79	4.9	416	1	ALAT_BOVIN	P34955	bos taurus	181	76	4.7	471	1	LEUB_CHRVO	Q7nub6	chromobacte
109	79	4.9	427	1	DSL1_CHICK	P34822	gallus gall	182	76	4.7	493	1	YEB6_YEAST	P39397	saccharomyc
110	79	4.9	510	1	GPMI_BACST	Q9x519	bacillus st	183	76	4.7	510	1	GPMI_BACSU	P19941	oryctolagus
111	79	4.9	637	1	DNAM_BUCAI	Q32464	buchnera ap	184	76	4.7	638	1	GHR_RABIT	Q13742	schizosacch
112	79	4.9	638	1	GHR_PIG	P19756	sus scrofa	185	76	4.7	805	1	VPHI_SCHPO	Q13094	meleagris g
113	78.5	4.9	409	1	DEOB_BUCAP	Q8x936	buchnera ap	186	76	4.7	831	1	PRLR_MELGA	Q8n224	streptococc
114	78.5	4.9	501	1	PD11_ARATH	Q9x101	arabidopsis	187	76	4.7	851	1	MUTS_STRP8	Q10366	schizosacch
115	78.5	4.9	559	1	MDL1_PRUDU	Q24243	prunus dulc	188	76	4.7	851	1	YDBG_SCHPO	Q8n224	streptococc
116	78.5	4.9	592	1	SYN2_HUMAN	Q92777	homo sapien	189	76	4.7	908	1	ACON_BACSU	R09339	bacillus su
117	78.5	4.9	600	1	DSBD_VIBCH	Q9kml1	vibrio chol	190	76	4.7	956	1	PODK_FLAPR	Q42736	flaviera pr
118	78.5	4.9	609	1	YL15_MYCLE	Q62132	mus musculus	191	76	4.7	1068	1	RBL1_HUMAN	P28749	homo sapien
119	78.5	4.9	656	1	PTPR_MOUSE	Q67178	aquifex aeo	192	76	4.7	1165	1	POL_GALV	P21414	gibbon ape
120	78.5	4.9	761	1	Y488_AQUAE	Q9byn7	homo sapien	193	75.5	4.7	222	1	TOXB_CLODI	P18177	clostridium
121	78.5	4.9	773	1	Z341_HUMAN	Q43115	arthrobacte	194	75.5	4.7	238	1	HIS5_STRCO	C92pw3	streptomyce
122	78.5	4.9	775	1	TREY_ARTSQ	Q44458	saccharomyc	195	75.5	4.7	312	1	LEXA_RHIME	Q1293	buchnera ap
123	78.5	4.9	1108	1	CYGE_RAT	P51840	rattus norv	196	75.5	4.7	394	1	TRPB_BUCBP	C31293	buchnera ap
124	78.5	4.9	1216	1	P1B1_RAT	P10687	rattus norv	197	75.5	4.7	466	1	LEU2_BUCTS	Q8xk25	vibrio para
125	78.5	4.9	4911	1	MLL1_HUMAN	Q8n524	homo sapien	198	75.5	4.7	510	1	GPMI_VIBPA	Q8xk25	clostridium
126	78	4.8	330	1	CAHX_FLABR	P46511	flaviera br	199	75.5	4.7	512	1	PDI_MEDSA	P21047	vaccinia vi
127	78	4.8	437	1	E2F1_HUMAN	Q01094	homo sapien	200	75.5	4.7	567	1	VE06_VACCC	P29828	medicago sa
128	78	4.8	485	1	GATA_BACST	Q931e2	bacillus st	201	75.5	4.7	732	1	ELM2_MOUSE	Q8bh15	mus musculu
129	78	4.8	532	1	Y400_YEAST	Q04458	saccharomyc	202	75.5	4.7	732	1	KDPD_CLOAB	P94608	clostridium
130	78	4.8	546	1	SYR_THEAC	Q9h1e7	thermoplasm	203	75.5	4.7	900	1	CARB_STRCO	Q9kxr6	streptomyce
131	78	4.8	638	1	DNAM_PESG	Q9wag9	pseudomonas	204	75.5	4.7	1102	1	PAS_HUMAN	P49327	homo sapien
132	78	4.8	644	1	DNAM_LSGPN	Q32482	legionella	205	75.5	4.7	2504	1	LEU2_BUCAI	P57150	buchnera ap
133	78	4.8	867	1	YQK1_CABEL	Q09285	caenorhabdi	206	75.5	4.7	142	1	RLI1_BUCAI	Q899m5	clostridium
134	78	4.8	902	1	IF2_BRAJA	Q89wa9	bradyrhizob	207	75	4.6	466	1	HOBI_SCHPO	Q74352	schizosacch
135	78	4.8	1010	1	PUR2_HUMAN	P22102	h trifunctio	208	75	4.6	466	1	LEU2_NEIMA	Q9ju82	neisseria m
136	78	4.8	1019	1	VP3_RDVF	P22102	h trifunctio	209	75	4.6	469	1	LEU2_NEIMB	Q91z15	neisseria m
137	77.5	4.8	256	1	HIS5_PASMU	Q9clm0	pasteurella	210	75	4.6	485	1	SYE_AGR15	Q8u785	agrobacteri
138	77.5	4.8	394	1	DEOB_BACAA	Q8lme0	bacillus an	211	75	4.6	553	1	YAGH_ECOLI	Q321f6	staphylococ
139	77.5	4.8	409	1	NER1_RAT	Q27126	methanobact	212	75	4.6	553	1	SYR_STAAN	Q9nw05	staphylococ
140	77.5	4.8	451	1	RP22_METTH	Q61234	mus musculus	213	75	4.6	562	1	SVR_THETN	Q8x786	thermoanaer
141	77.5	4.8	503	1	SNAI_MOUSE	P48452	bos taurus	214	75	4.6	566	1	DCPY_EMENI	P87208	emericeila
142	77.5	4.8	521	1	P2BA_BOVIN	Q08209	homo sapien	215	75	4.6	711	1	SEF2_ARATH	Q23141	arabidopsis
143	77.5	4.8	521	1	ESTB_DROMI	O16170	drosophila	216	75	4.6	922	1	DFOI_RICFE	Q23141	arabidopsis
144	77.5	4.8	545	1	ESTB_DROMI	O16170	drosophila	217	75	4.6	1244	1	YPA2_HUMAN	Q29317	homo sapien
145	77.5	4.8	567	1	VE06_VACCV	P25726	vaccinia vi	218	75	4.6	1391	1	YPA2_HUMAN	Q9441	caenorhabdi
146	77.5	4.8	579	1	Y359_CHLMU	P21607	chlamydia m	219	75	4.6	1391	1	YPA2_HUMAN	P78013	mycoplasma
147	77.5	4.8	609	1	YL15_MYCTU	Q33250	mycobacteri	220	75	4.6	3866	1	HEX_MOUSE	P55200	mus musculu
148	77.5	4.8	656	1	PTPR_RAT	O08617	rattus norv	221	75	4.6	242	1	NAGE_MYCPE	Q8ewm7	mycoplasma
149	77.5	4.8	801	1	SYFB_STRP3	Q8k820	streptococc	222	75	4.6	255	1	RS2_LACLA	Q8cd4	lactococcus
150	77.5	4.8	1067	1	TR11_STRCO	Q9de2	streptomyce	223	75	4.6	257	1	TARA_BACSU	Q8k17	bacillus su
151	77.5	4.8	175	1	LPNN_MYCTU	Q50693	mycobacteri	224	75	4.6	366	1	VE2_RHPV1	P22156	rhesus papi
152	77	4.8	403	1	E2F1_CHICK	Q90977	gallus gall	225	75	4.6	468	1	6PGD_STRAP	Q8cp47	staphylococ
153	77	4.8	404	1	GAT5_MOUSE	P97489	mus musculus	226	75	4.6	487	1	WMSA_BACSU	P42417	bacillus su
154	77	4.8	528	1	GYRA_MYCKA	Q57118	frankia aln	227	75	4.6	492	1	ALG8_AZOVI	P94199	azotobacter
155	77	4.8	631	1	MX1_MOUSE	Q49608	mycobacteri	228	75	4.6	504	1	APAG_ECOLI	P08531	escherichia
156	77	4.8	878	1	IL3B_MOUSE	P09922	mus musculus	229	75	4.6	510	1	GPMI_CLOBR	Q97153	clostridium
157	77	4.8	1643	1	RPPO_NMV	P26954	mus musculus	230	74.5	4.6	513	1	LEU1_LACLA	Q02141	lactococcus
158	77	4.8	170	1	TONB_PSEAE	P26954	mus musculus	231	74.5	4.6	513	1	LEU1_LACLA	Q82156	salmonella
159	76.5	4.7	342	1	DEOB_THETN	P15095	narcissus m	232	74.5	4.6	693	1	IF2_CLOAB	Q97151	clostridium
160	76.5	4.7	393	1	KDOT_CHLMU	Q9nph6	homo sapien	233	74.5	4.6	710	1	ETF2_VARV	P33806	variola vir
161	76.5	4.7	430	1	NIFD_METTL	Q51368	pseudomonas	234	74.5	4.6	715	1	2P2_CANPA	P47983	canis famil
162	76.5	4.7	478	1	CPCU_RABIT	Q9k158	thermoanaer	235	74.5	4.6	729	1	NTT7_BOVIN	Q9x559	bos taurus
163	76.5	4.7	489	1	GPMI_SYNEL	Q8n224	streptococc	236	74.5	4.6	987	1	YD94_METUA	Q58789	methanococ
164	76.5	4.7	531	1	INAI_TRIHA	P20620	methanococc	237	74.5	4.6	1063	1	RBL1_MOUSE	P64701	mus musculu
165	76.5	4.7	573	1	RHBC_RHIME	Q9nph6	homo sapien	238	74.5	4.6	1178	1	PHB1_YEAST	P27395	j genome po
166	76.5	4.7	585	1	ETF2_VACCC	P59177	synchococc	239	74.5	4.6	3432	1	POLG_JAEV1	P19110	j genome po
167	76.5	4.7	710	1	ETF2_VACCC	P59177	synchococc	240	74.5	4.6	3432	1	POLG_JAEV5	P32886	j genome po
168	76.5	4.7	710	1	ETF2_VACCC	Q923r0	rhizobium m	241	74.5	4.6	3432	1	POLG_JAEV5	P46281	flaviera pr
169	76.5	4.7	710	1	ETF2_VACCC	Q57220	vaccinia vi	242	74.5	4.6	329	1	CAHX_FLAPR	Q46281	flaviera pr
170	76.5	4.7	710	1	ETF2_VACCC	P20635	vaccinia vi	243	74.5	4.6	380	1	APG2_ARCFU	O28847	archaeoglob
171	76.5	4.7	710	1	ETF2_VACCC	P20636	vaccinia vi	244	74.5	4.6					
172	76.5	4.7	982	1	MSHM_SARGL	Q63852	sarcophyton	245	74.5	4.6					
173	76.5	4.7	1064	1	CARB_LACLA	Q9cfv2	lactococcus	246	74.5	4.6					
174	76.5	4.7	1274	1	MYPC_HUMAN	O14896	homo sapien	247	74.5	4.6					
175	76.5	4.7	1616	1	RRFO_TOMS1	Q9yk46	tomato mosa	248	74.5	4.6					
176	76	4.7	322	1	NADA_AQUAE	O87730	aquifex aeo	249	74.5	4.6					
177	76	4.7	345	1	YA03_TREFA	O83968	treponema p	250	74	4.6					
178	76	4.7	376	1	MED7_SCHPO	O60104	schizosacch	251	74	4.6					
179	76	4.7	431	1	HISX_VIBVU	Q8d8q0	vibrio vuln	252	74	4.6					

253	74	4.6	442	1	ENOA_LACPL	Q88yh3	lactobacill	326	72.5	4.5	663	1	RGPI_YEAST	P16664	saccharomyc
254	74	4.6	474	1	VP61_NPVOP	O10270	orgyia pseu	327	72.5	4.5	801	1	SYFB_STRPY	Q9a010	streptococc
255	74	4.6	502	1	P2BC_HUMAN	P48454	homo sapien	328	72.5	4.5	878	1	ACON_RICCN	Q92990	rickettsia
256	74	4.6	504	1	MATK_ACTDE	Q95bz7	actinidia d	329	72.5	4.5	885	1	PODK_ENTHI	P37213	ricettameba h
257	74	4.6	508	1	PD12_ARATH	Q9sxg3	arabidopsis	330	72.5	4.5	1091	1	DIA_DROME	P48608	drosophila
258	74	4.6	521	1	GPM1_METMA	Q8pyf8	methanosarc	331	72.5	4.5	1556	1	Y934_HUMAN	Q9y2e4	homo sapien
259	74	4.6	607	1	MM16_HUMAN	P51512	homo sapien	332	72.5	4.5	1616	1	RRPO_TOMK1	Q9qlt8	tomato mosa
260	74	4.6	611	1	GLGE_FUSNN	Q8rf62	fusobacteri	333	72.5	4.5	1616	1	RRPO_TOMK2	P89676	tomato mosa
261	74	4.6	621	1	ILVB_MYCAV	Q59498	mycobacteri	334	72.5	4.5	1616	1	RRPO_TOML	P03587	tomato mosa
262	74	4.6	636	1	DNAX_PHOLL	Q7n8y4	photorhabdi	335	72.5	4.5	1675	1	CLH1_HUMAN	Q06101	homo sapien
263	74	4.6	638	1	DNAX_BUCAP	Q8k9v8	buchnera ap	336	72.5	4.5	1675	1	CLH1_BOVIN	P49951	bos taurus
264	74	4.6	640	1	DNAX_VIBHA	Q87384	vibrio havy	337	72.5	4.5	1675	1	CLH1_RAT	P11442	rattus norv
265	74	4.6	709	1	SUL1_CABEL	Q21376	caenorhabdi	338	72.5	4.5	2004	1	MYSE_HUMAN	Q92794	homo sapien
266	74	4.6	850	1	DPO1_ANATH	Q59156	anaerocellu	339	72.5	4.5	2222	1	DPOE_YEAST	P21951	saccharomyc
267	74	4.6	953	1	PODK_FLABI	Q93735	flaveria bi	340	72.5	4.5	2319	1	FAB_MOUSE	Q86194	mus musculu
268	74	4.6	960	1	FTSK_VIBCH	Q84133	flaveria chol	341	72.5	4.5	3175	1	RPOA_EAV	P19811	equine arte
269	74	4.6	1121	1	BMS1_SCHPO	Q94653	schizosacch	342	72.5	4.5	4367	1	DYHC_NEUCR	P45443	neurospora
270	74	4.6	1423	1	FRUA_STRMU	Q03174	streptococc	343	72	4.5	330	1	CAH1_FLALI	P46512	flaveria li
271	74	4.6	1447	1	BUDA_YEAST	Q47136	saccharomyc	344	72	4.5	357	1	FUL1_ACHFU	P35905	a fulicin p
272	74	4.6	4829	1	BIR6_HUMAN	Q9nr09	homo sapien	345	72	4.5	358	1	T3H2_HABPA	P36433	haemophilus p
273	73.5	4.5	146	1	HBB2_NAJNA	P22143	naja naja	346	72	4.5	359	1	RS22_SPICI	P19679	spiroplasma
274	73.5	4.5	208	1	YCAC_ECOLI	P21367	escherichia	347	72	4.5	386	1	YA66_METUA	Q58466	methanococc
275	73.5	4.5	298	1	PNPP_SCHPO	Q00472	schizosacch	348	72	4.5	392	1	DEOB_STAM	Q99x76	staphylococ
276	73.5	4.5	397	1	UXUA_YERPE	Q8zdk8	yersinia pe	349	72	4.5	395	1	DEOB_MYCFU	Q98qt4	mycoplasma
277	73.5	4.5	416	1	APMA_HUMAN	Q9hdc9	homo sapien	350	72	4.5	426	1	SCB1_MOUSE	Q9z219	mus musculu
278	73.5	4.5	447	1	G3PE_ARATH	P25857	arabidopsis	351	72	4.5	461	1	GLMU_BUCAP	Q8ka74	buchnera ap
279	73.5	4.5	488	1	GATA_OEITH	Q8es78	oceanobacil	352	72	4.5	464	1	LEU2_BACTN	Q8a617	bacteroides
280	73.5	4.5	505	1	GPM1_STAAW	Q99vk6	staphylococ	353	72	4.5	484	1	PEPD_ECOLI	P35288	escherichia
281	73.5	4.5	505	1	GPM1_STAAW	Q8ncl5	staphylococ	354	72	4.5	491	1	HSF1_CHICK	P36229	gallus gall
282	73.5	4.5	505	1	GPM1_STAEP	Q8cpv4	staphylococ	355	72	4.5	500	1	CPDK_MESAU	Q9gyg5	mesocricetu
283	73.5	4.5	514	1	GPM1_ECO57	Q8xde9	escherichia	356	72	4.5	510	1	GPM1_VIBU	Q8dcw1	vibrio vuln
284	73.5	4.5	514	1	GPM1_ECOLI	P37689	escherichia	357	72	4.5	607	1	MM16_MOUSE	Q9wt0	mus musculu
285	73.5	4.5	514	1	GPM1_SALTI	Q8z2f0	salmonella	358	72	4.5	607	1	MM16_RAT	Q35548	rattus norv
286	73.5	4.5	542	1	GPM1_SHIFL	P59176	shigella fl	359	72	4.5	626	1	PPOC_LYCES	Q08305	lycopersico
287	73.5	4.5	542	1	GPM1_SHIFL	P47982	drosophila	360	72	4.5	634	1	PPOA_LYCES	Q08303	lycopersico
288	73.5	4.5	544	1	EST6_DROME	P08171	drosophila	361	72	4.5	634	1	GHR_BOVIN	P73108	bos taurus
289	73.5	4.5	544	1	ETF2_VACCT	Q9j793	vaccinia vi	362	72	4.5	656	1	DNLJ_HELPY	Q25336	heleobacte
290	73.5	4.5	710	1	FTSK_VIBPA	Q87gp4	vibrio para	363	72	4.5	851	1	MUTS_STRPY	Q99x18	streptococc
291	73.5	4.5	1028	1	RSGI_BOVIN	P09851	bos taurus	364	72	4.5	939	1	A2A2_HUMAN	Q94973	h adapter-r
292	73.5	4.5	1071	1	CARE_NEIGO	Q59599	neisseria g	365	72	4.5	1036	1	YAN2_SCHPO	O10068	schizosacch
293	73.5	4.5	1111	1	SEC8_NEUCR	Q9he88	neurospora	366	72	4.5	1064	1	JWJ2_HUMAN	O75164	homo sapien
294	73.5	4.5	1944	1	ANCI_MOUSE	P53395	mus musculu	367	72	4.5	1129	1	YB95_YEAST	P81021	saccharomyc
295	73.5	4.5	2849	1	Pili_HUMAN	Q8txc9	homo sapien	368	72	4.5	1270	1	VGLN_CHICK	P81021	gallus gall
296	73.5	4.5	6684	1	R1AB_CVPPU	Q91w06	p replicase	369	72	4.5	1443	1	DPO3_MYCPN	P75080	mycoplasma
297	73	4.5	470	1	VL2_Hpv39	P24939	human papil	370	72	4.5	1502	1	N170_YEAST	P38181	saccharomyc
298	73	4.5	500	1	CPDE_MESAU	Q9qvg6	mesocricetu	371	72	4.5	1516	1	Y819_PSEAE	Q9hvt2	pseudomonas
299	73	4.5	535	1	Y912_METMA	Q8pf0	methanosarc	372	72	4.5	2283	1	DPOE_MOUSE	Q9wvf7	mus musculu
300	73	4.5	533	1	GPM1_ANASP	Q8pyl2	anabaena sp	373	72	4.5	4344	1	DYHC_EWENI	P45444	emericeia
301	73	4.5	564	1	FEPI_SCHPO	Q10134	schizosacch	374	71.5	4.4	241	1	NAGE_CLOAB	Q97mk9	clostridium
302	73	4.5	578	1	MDLB_BUCBP	Q10134	schizosacch	375	71.5	4.4	243	1	GCHI_YEAST	P51601	saccharomyc
303	73	4.5	618	1	ILVB_MYCTU	Q89a96	buchnera ap	376	71.5	4.4	261	1	YAC7_YEAST	P39735	saccharomyc
304	73	4.5	635	1	DNAX_VIBCH	O53250	mycobacteri	377	71.5	4.4	273	1	Y133_METUA	Q57597	methanococc
305	73	4.5	649	1	DXS1_KITGR	O34241	vibrio chol	378	71.5	4.4	317	1	KPRS_BRAJA	Q89dj1	bradyrhizob
306	73	4.5	738	1	ZN84_HUMAN	Q9fiv2	kitasatospo	379	71.5	4.4	329	1	CCPA_STAXY	Q56194	staphylococ
307	73	4.5	1057	1	VF2_AHSV3	P51523	homo sapien	380	71.5	4.4	343	1	RADA_HALVO	Q48328	halobacteri
308	73	4.5	1076	1	CARB_ARCFU	Q89508	african hor	381	71.5	4.4	394	1	DEOB_EACSU	P45353	bacillus su
309	73	4.5	1125	1	PHYA_POPTM	O28994	archaeoglob	382	71.5	4.4	465	1	LEU2_EUCFS	P58945	buchnera ap
310	73	4.5	3063	1	CALC_HUMAN	O49934	populus tre	383	71.5	4.4	484	1	PEN3_ADEP3	Q84176	porcine ade
311	73	4.5	4594	1	DYHC_HUMAN	Q99715	homo sapien	384	71.5	4.4	495	1	E1BL_ADE02	Q32444	human adeno
312	73	4.5	4644	1	DYHC_RAT	O14204	homo sapien	385	71.5	4.4	515	1	GPM1_YERPE	Q8zjnl0	yersinia pe
313	72.5	4.5	223	1	VZL2_EBV	P38650	rattus norv	386	71.5	4.4	562	1	NKX2_HUMAN	Q60749	homo sapien
314	72.5	4.5	258	1	HIS6_KLEOX	P03205	epstein-bar	387	71.5	4.4	567	1	V506_VARV	Q9mpa2	homo sapien
315	72.5	4.5	315	1	TRER_SALTY	F45603	kieseliella	388	71.5	4.4	567	1	V506_VARV	P33619	variola vir
316	72.5	4.5	385	1	OXDC_BACSU	P36674	salmonella	389	71.5	4.4	600	1	IF2P_SULSO	Q980q8	sulfobolus
317	72.5	4.5	436	1	HISX_DEIRA	O34714	bacillus su	390	71.5	4.4	616	1	MUTA_STRCM	Q05064	streptomyce
318	72.5	4.5	505	1	GPM1_AGRTS	Q9rsi4	deinococcus	391	71.5	4.4	663	1	GR78_SCHPO	P36604	schizosacch
319	72.5	4.5	537	1	SYR_MYCPN	Q8uaa5	agrobacteri	392	71.5	4.4	816	1	SUS2_ORYSA	P31924	oryza sativ
320	72.5	4.5	555	1	EST4_DROMI	P75222	mycoplasma	393	71.5	4.4	887	1	OBP_HSVB	P28947	equine herp
321	72.5	4.5	564	1	ASMI_CABEL	O16168	drosophila	394	71.5	4.4	893	1	NIA_LBPMC	P36842	leptospheer
322	72.5	4.5	575	1	MIS_BOVIN	Q10916	caenorhabdi	395	71.5	4.4	899	1	POL_MMTVB	P33365	mouse mamma
323	72.5	4.5	606	1	MM17_HUMAN	Q9u1z9	homo sapien	396	71.5	4.4	985	1	AGLU_ASPOR	Q12558	aspergillus
324	72.5	4.5	617	1	FXK1_MOUSE	P42128	mus musculu	397	71.5	4.4	1006	1	BGAL_ASPNG	P29853	aspergillus
325	72.5	4.5	643	1	DNAX_CANBF	Q7vql4	candidatus	398	71.5	4.4	1014	1	FTK2_NEIMA	Q9juk9	neisseria m

399	71.5	4.4	1420	1	APX_XENLA	Q01613 xenopus lae
400	71.5	4.4	1447	1	DCC_HUMAN	P43146 homo sapien
401	71.5	4.4	2080	1	TOXC_COCCA	Q92215 c putative
402	71.5	4.4	3140	1	POLG_PPVRA	P17767 p genome po
403	71.5	4.4	3141	1	POLG_PPVD	P13529 p genome po
404	71.5	4.4	3830	1	SACS_MOUSE	Q9jfc8 mus musculus
405	71.5	4.4	4644	1	DYHC_MOUSE	Q9jhu4 mus musculus
406	71	4.4	286	1	PARB_CHLPN	Q9z7m0 chlamydia p
407	71	4.4	288	1	ACCD_PORPU	P51198 porphyra pu
408	71	4.4	309	1	VOGH_BACSU	P46339 bacillus su
409	71	4.4	325	1	HMGL_RAT	P97519 rattus norv
410	71	4.4	327	1	PLSG_THEMEA	Q9wxz6 thermotoga
411	71	4.4	396	1	TRPB_ECO57	Q8x7b6 escherichia
412	71	4.4	396	1	TRPB_ECOL6	Q8fhv9 escherichia
413	71	4.4	396	1	TRPB_ECOLI	P00932 escherichia
414	71	4.4	407	1	DEOB_ECOLI	P07651 escherichia
415	71	4.4	412	1	AIAT_MUSCR	P26595 mus caroli
416	71	4.4	432	1	ENO_ENTHR	Q8g770 enterococcu
417	71	4.4	437	1	ORPI_MOUSE	Q91x19 mus musculus
418	71	4.4	473	1	SYC_METWA	Q8pvg1 methanosarc
419	71	4.4	509	1	NRM3_ARATH	Q9snv9 arabidopsis
420	71	4.4	510	1	GPMI_VIBCH	Q9kv22 vibrio chol
421	71	4.4	558	1	GGTI_RAT	P07314 rattus norv
422	71	4.4	579	1	COE2_BRABE	Q93375 brachydanio
423	71	4.4	585	1	SYR_AGR15	Q8uep4 agrobacteri
424	71	4.4	585	1	TFHI_DROME	Q96e68 drosophila
425	71	4.4	621	1	APS_MOUSE	Q9jld9 mus musculus
426	71	4.4	682	1	REGC_BACSU	Q34942 bacillus su
427	71	4.4	777	1	LON_EUCAI	P57549 buchnera ap
428	71	4.4	875	1	SYL_RHILO	Q98eu7 rhizobium l
429	71	4.4	1027	1	ISWI_DROME	Q24368 drosophila
430	71	4.4	1132	1	BATS_HUMAN	P46379 homo sapien
431	71	4.4	1197	1	EVGS_ECOLI	P30855 escherichia
432	71	4.4	1401	1	LATA_LATMA	P23631 latrodectus
433	71	4.4	4639	1	DYHC_DROME	P37276 drosophila
434	70.5	4.4	146	1	HBB_MESAU	P02094 mesocricetu
435	70.5	4.4	178	1	VE7I_METJA	Q58866 methanococc
436	70.5	4.4	333	1	GIPC_RAT	Q92254 rattus norv
437	70.5	4.4	343	1	EXB_THEMEA	Q9x013 thermotoga
438	70.5	4.4	352	1	TX37_CABEL	Q9uzc9 caenorhabdi
439	70.5	4.4	353	1	TPO_HUMAN	P40225 homo sapien
440	70.5	4.4	378	1	KLP2_BOMMO	P46874 bombyx mori
441	70.5	4.4	388	1	DEOB_DEIRA	Q9rsi9 deinococcus
442	70.5	4.4	393	1	DEOB_BACST	Q24821 bacillus st
443	70.5	4.4	401	1	CGBI_ORXJA	Q9dea0 oryzias jav
444	70.5	4.4	441	1	GDFP_MOUSE	Q07105 mus musculus
445	70.5	4.4	449	1	NIR_DROME	P25331 drosophila
446	70.5	4.4	494	1	VPE_CITSI	P49043 citrus sine
447	70.5	4.4	508	1	C6D5_DROME	Q9vfp1 drosophila
448	70.5	4.4	514	1	T3RH_HABIN	P44105 haemophilus
449	70.5	4.4	527	1	MM19_MOUSE	Q9jhi0 mus musculus
450	70.5	4.4	529	1	HSFI_HUMAN	Q00613 homo sapien
451	70.5	4.4	531	1	VTGF_LACLA	Q9ce82 lactococcus
452	70.5	4.4	585	1	ESRI_ORENI	Q9y3h3 oreochromis
453	70.5	4.4	608	1	GHR_CHICK	Q02092 gallus gall
454	70.5	4.4	613	1	TX18_MOUSE	Q9ep26 mus musculus
455	70.5	4.4	657	1	PTPR_HUMAN	Q15256 homo sapien
456	70.5	4.4	658	1	VATI_METTH	Q27041 methanobact
457	70.5	4.4	805	1	TERA_XENLA	P23787 xenopus lae
458	70.5	4.4	914	1	SYA_PYRPU	Q8u425 pyrococcus
459	70.5	4.4	961	1	ACON_MYCAV	Q08451 mycobacteri
460	70.5	4.4	1382	1	INSR_HUMAN	P06213 homo sapien
461	70.5	4.4	1625	1	CTPI_MYCTU	Q10900 mycobacteri
462	70.5	4.4	2738	1	PGCV_RAT	Q9erb4 rattus norv
463	70.5	4.4	4377	1	ANK3_HUMAN	Q12955 homo sapien
464	70	4.3	187	1	RL5_MYCTU	P95064 mycobacteri
465	70	4.3	236	1	Y141_METTH	Q02644 methanobact
466	70	4.3	249	1	YF82_METJA	Q58977 methanococc
467	70	4.3	260	1	ARGT_SALTY	P02911 salmonella
468	70	4.3	364	1	PLCE_HUMAN	Q9nuq2 homo sapien
469	70	4.3	386	1	SUCC_DEIRA	Q9ruy3 deinococcus
470	70	4.3	390	1	TGFI_HORSE	Q19011 equus cabal
471	70	4.3	397	1	APGM_METWA	Q8px04 methanosarc

ALIGNMENTS

RESULT 1		ID_YA93_SCHPO	STANDARD;	PRT;	758 AA.
AC	Q09782;	OC	Q09782;		
DT	01-NOV-1995 (Rel. 32, Created)	DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)	DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DE	Hypothetical protein C13G6.03 in chromosome 1.	DE	Hypothetical protein C13G6.03 in chromosome 1.		
GN	SPAC13G6.03.	GN	SPAC13G6.03.		
OS	Schizosaccharomyces pombe (Fission yeast).	OS	Schizosaccharomyces pombe (Fission yeast).		
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;	OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;		
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;	OC	Schizosaccharomycetales; Schizosaccharomycetaceae;		
OC	Schizosaccharomycetes.	OC	Schizosaccharomycetes.		
OX	NCBI_taxid=4896;	OX	NCBI_taxid=4896;		
RN	[1]	RN	[1]		
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.		
RC	STRAIN=972;	RC	STRAIN=972;		
RX	MEDLINE=21848401; PubMed=11859360;	RX	MEDLINE=21848401; PubMed=11859360;		
RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,	RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,		
RA	Sgourou J., Beal N., Hayes J., Baker S., Basham D., Bowman S.,	RA	Sgourou J., Beal N., Hayes J., Baker S., Basham D., Bowman S.,		
RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,	RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,		
RA	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,	RA	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,		
RA	Gentles S., Goble A., Hamlin N., Harris D., Hidaigo J., Hodgson G.,	RA	Gentles S., Goble A., Hamlin N., Harris D., Hidaigo J., Hodgson G.,		
RA	Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,	RA	Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,		
RA	James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,	RA	James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,		
RA	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,	RA	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,		
RA	Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,	RA	Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,		
RA	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,	RA	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,		
RA	Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,	RA	Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,		
RA	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren I., Whitehead S.,	RA	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren I., Whitehead S.,		
RA	Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,	RA	Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,		
RA	Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,	RA	Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,		
RA	Gabel C., Fuchs M., Fritz C., Holzer E., Reinhardt R., Pohl T.M.,	RA	Gabel C., Fuchs M., Fritz C., Holzer E., Reinhardt R., Pohl T.M.,		
RA	Borzum K., Langer I., Beck A., Lehmach H., Reinhardt R., Pohl T.M.,	RA	Borzum K., Langer I., Beck A., Lehmach H., Reinhardt R., Pohl T.M.,		
RA	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,	RA	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,		
RA	Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,	RA	Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,		
RA	Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,	RA	Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,		
RA	Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Rhode G.,	RA	Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Rhode G.,		
RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,	RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,		


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RESULT 3
PICO MOUSE
ID -PICO_MOUSE STANDARD; PRT; 1093 AA.
AC Q9JUI6; Q9CRY2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphatidylinositol-glycan biosynthesis, class O protein (PIG-O).
GN PIGO
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
RC TISSUE=Testis;
RX MEDLINE=20347191; PubMed=10781593;
RA Hong Y., Maeda Y., Watanabe R., Inoue N., Ohishi K., Kinoshita T.;
RT "Requirement of PIG-F and PIG-O for transferring phosphoethanolamine to
RL the third mannose in glycosylphosphatidylinositol.";
RN [2]
RP SEQUENCE OF 931-1101 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryonic head;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadori K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA Schirni L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: Involved in GPI-anchor biosynthesis but not essential
CC for this process. Involved, together with PIGF, in the transfer of
CC ethanolamine phosphate to the third mannose of GPI.
CC -!- PATHWAY: GPI-anchor biosynthesis.
CC -!- SUBUNIT: Forms a complex with PIGF. PIGF is required to stabilize
CC PIGO.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum.
CC
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CC or send an email to license@isb-sib.ch.
CC
CC EMBL; AB038560; BAA96254.1; ALT INIT.
CC EMBL; AK013913; BAB29052.1; --
CC MGD; MG11861452; Pigo.
CC GO; GO:0005789; C:endoplasmic reticulum membrane; IDA.
CC GO; GO:0008508; P:GPI anchor biosynthesis; IDA.
CC InterPro; IPR002591; Phosphodiect.
CC Pfam; PF01663; Phosphodiect; 1.
CC GPI-anchor biosynthesis; Transmembrane; Endoplasmic reticulum.
CC FT TRANSMEM 4 24 POTENTIAL.
CC FT TRANSMEM 460 480 POTENTIAL.
CC FT TRANSMEM 483 503 POTENTIAL.

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FT TRANSMEM 512 532 POTENTIAL.
FT TRANSMEM 669 689 POTENTIAL.
FT TRANSMEM 702 722 POTENTIAL.
FT TRANSMEM 748 768 POTENTIAL.
FT TRANSMEM 831 851 POTENTIAL.
FT TRANSMEM 856 876 POTENTIAL.
FT TRANSMEM 945 965 POTENTIAL.
FT TRANSMEM 1018 1038 POTENTIAL.
FT TRANSMEM 1052 1072 POTENTIAL.
FT TRANSMEM 1000 1000 V -> M (IN REF. 2).
SQ SEQUENCE 1093 AA; 119156 MW; AB641F9F3527296C CRC64;

Query Match 30.3%; Score 490; DB 1; Length 1093;
Best Local Similarity 40.5%; Pred. No. 2.1e-33;
Matches 118; Conservative 41; Mismatches 108; Indels 24; Gaps 7;

QY 19 GIADVFLRGFPFPAVRSSARAHGAEP-PAPEPSAGASSNNWTTLPPLFSKVIVLIDALR 77
DB 20 GIALFTSGFLLTRELTNQSSCQELPGPGPLPWGSHGKPGACWMPGRFRSRVVLVLDALR 79
QY 78 DDF-----VFGSKGVKFMPTTYL-----VEKGASHS--FVAEAKPPTVTPRIKAL 122
DB 80 FDFAPQPSRSHVPGPPVS-VFPLKGLSLQRILESOPHGLRYSQVDPPTTMMQLKAL 138
QY 123 MTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRVFYGDETWKLFPPKHFVEYDGTTS 182
DB 139 TTGSLPTFDAGSNFASHAIVEDNVLIQLNSAGRRVVGDDTWRDLFGAFSAQAFPESS 198
QY 183 FFVSDYTDVDMNTRHLDKVLKGDWDLILHVLGDLHTGHISGPNPLIGQKLSMDSV 242
DB 199 FNVRLDHTVDNGLEHLHYPTLDGGSWDVLTIAHFLGVDHCHGKHGPHHPMAKLSQMDQV 258
QY 243 LMKIHTSLOKSERETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLIIS 293
DB 259 IQGL---IERLENDT----LLVAGDHGMWNGDHGDSLEVSAAFLYS 302

RESULT 4
PICO HUMAN
ID -PICO_HUMAN STANDARD; PRT; 1088 AA.
AC O8TEQ8; O8TDS8; O96CS9; O9BVN9; Q9V4B0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Phosphatidylinositol-glycan biosynthesis, class O protein (PIG-O).
GN PIGO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RA Ansoorge W., Winkner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
RT "The nucleotide sequence of a long cDNA clone isolated from human
RT spleen.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Ganes J., Danganan L., Poundstone P.,
RA Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T.,
RA Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
RA Bruce R., Thomas P., Quan G., Krommiller B., Atrellano A.,
RA Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
RA Carrano A.V.;
RT "Sequence analysis of a human P1 clone containing the XRCC9 DNA repair

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 2, 2004, 16:24:48 ; Search time 53 Seconds

(without alignments)
1652.636 Million cell updates/sec

Title: US-10-036-150-45

Perfect score: 1617

Sequence: 1 MELGSGTATCCVAIEVLGI.....LISSAFERKPGDIRPKHVQ 310

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1617	100.0	310	4	Aay72877 Human PRO
3	1617	100.0	310	4	Aab87595 Human PRO
4	1617	100.0	310	5	Aau83650 Human PRO
5	1617	100.0	310	5	Abg95920 Human sec
6	1617	100.0	310	5	Abb84962 Human PRO
7	1617	100.0	310	5	Abb95568 Human ang
8	1617	100.0	310	6	Abu69112 Human PRO
9	1617	100.0	310	6	Abu80797 Human PRO
10	1617	100.0	310	6	Abu33763 Novel hum
11	1617	100.0	310	6	Abu90945 Novel hum
12	1617	100.0	310	6	Abu34004 Human sec
13	1617	100.0	310	6	Abu19428 Human sec
14	1617	100.0	310	6	Abu72021 Novel hum
15	1617	100.0	310	6	Abu71575 Human sec
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17	1617	100.0	310	6	Abg74761 Human PRO
18	1617	100.0	310	6	Abu69089 Human PRO
19	1617	100.0	310	6	Abu91029 Human PRO
20	1617	100.0	310	6	Abu27350 Human sec
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22	1617	100.0	310	6	Abu81215 Human sec
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96	1617	100.0	310	8	ADE41542	Human sec
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102	1617	100.0	310	8	ADD74327	Human PRO	175	481	29.7	1089	6	ABR66879	Human sec
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112	1617	100.0	310	8	ADD85303	Novel hum	185	481	29.7	1089	6	ABU95341	Novel hum
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521	481	29.7	1089	6	ABM11374	Human sec
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531	481	29.7	1089	6	ABO38059	Human sec
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533	481	29.7	1089	6	ABM66772	Human sec
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ALIGNMENTS

RESULT 1

ID AAB18918 standard; protein; 310 AA.

XX AAB18918;

XX 08-FEB-2001 (first entry)

XX A novel polypeptide designated PRO4405.

XX Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;
 KW PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;
 KW PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;
 KW PRO4424; PRO4423; PRO4430; PRO4499; tumour; obesity; diabetes;
 KW insulinemia; kidney disorder; Bergers disease; nephropathy;
 KW Schonelein-Henoch purpura; celiac disease; dermatitis herpetiformis;
 KW Crohns disease.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX Peptide 1..34
 FT Modified-site /note= "signal peptide"
 FT Modified-site 6..12
 FT Modified-site /note= "N-myristoylation site"
 FT Modified-site 52..58
 FT Modified-site /note= "N-myristoylation site"
 FT Modified-site 56..60
 FT Domain /note= "N-glycosylation site"
 FT Domain 58..76
 FT /note= "transmembrane domain"

FT Modified-site /note= "N-myristoylation site"
 FT 154..158
 FT /note= "Amidation site"
 FT 194..198
 FT Modified-site /note= "Asn is N-glycosylated"
 FT 205..208
 FT Binding-site /note= "Cell attachment sequence"
 FT 233..239
 FT Modified-site /note= "N-myristoylation site"
 FT 270..276
 FT Modified-site /note= "N-myristoylation site"
 FT 275..281
 FT Modified-site /note= "N-myristoylation site"
 FT 278..284
 FT Modified-site /note= "N-myristoylation site"
 XX WO200116319-A2.
 XX 08-MAR-2001.
 XX 23-AUG-2000; 2000WO-US023522.
 XX 31-AUG-1999; 99US-01517133P.
 XX 01-SEP-1999; 99WO-US020111.
 XX 16-DEC-1999; 99WO-US030095.
 XX 18-FEB-2000; 2000WO-US004342.
 XX 01-MAR-2000; 2000WO-US005601.
 XX 30-MAR-2000; 2000WO-US008439.
 XX 17-MAY-2000; 2000WO-US013705.
 XX 22-MAY-2000; 2000WO-US014042.
 XX 30-MAY-2000; 2000WO-US014941.
 XX 05-JUN-2000; 2000US-0209832P.
 XX (GETH) GENENTECH INC.
 XX Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Tumas D;
 PI Watanabe CK, Wood WI;
 PI WPI; 2001-226690/23.
 DR N-PSDB; AAD02923.
 XX New PRO polypeptides for treating immune related and inflammatory
 PT diseases such as rheumatoid arthritis, systemic vasculitis, asthma,
 PT autoimmune hemolytic anemia, and diabetes mellitus.
 XX Claim 10; Fig 8; 118pp; English.
 XX The present sequence is PRO4405 protein encoded by DNA84920-2614 cDNA
 CC clone. PRO protein, its agonist or antagonist or its antibody which are
 CC capable of enhancing or inhibiting the proliferation of T-lymphocytes or
 CC of increasing the infiltration of inflammatory cells into a tissue are
 CC useful in the diagnosis and treatment of immune-related diseases in
 CC mammals. The PRO protein is useful for treating systemic lupus
 CC erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
 CC arthritis, spondyloarthritis, systemic sclerosis, idiopathic
 CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
 CC sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia,
 CC thyroiditis, diabetes mellitus, immune-mediated renal disease,
 CC demyelinating disease of the central or peripheral nervous system,
 CC idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, chronic
 CC inflammatory demyelinating polyneuropathy, hepatobiliary disease,
 CC infectious or autoimmune chronic active hepatitis, primary biliary
 CC cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory
 CC bowel disease, gluten-sensitive enteropathy, Whipple's disease,
 CC autoimmune or immune-mediated skin diseases such as bullous skin disease,
 CC erythema multiforme and contact dermatitis, psoriasis, allergic diseases
 CC such as asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity and urticaria immunologic diseases of the lung such as
 CC eosinophilic pneumonitis, idiopathic pulmonary fibrosis, hyper-
 CC sensitivity pneumonitis, transplantation associated diseases such as
 CC graft rejection or graft-versus-host-disease
 XX Sequence 310 AA;

Query Match 100.0%; Score 1617; DB 4; Length 310;
 Best Local Similarity 100.0%; Pred. No. 4.6e-159;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 NRLSGTATCCCAIEVLGIAVFLRGFPAPVRSSARAEGHGAEPPEPSAGASSNWTL 60
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 DB 61 PPPLFSKWIVLIDALRDDDFVFGSKGVKFWPYTYLVKKGASHSFVAEAKPPTVTPRIK 120
 QY 121 ALMTGSLPGFVDVIRNLNSPALLEDSDSVIRQAAGKRIIVFYGDETWKLPKHFVEYDGT 180
 DB 121 ALMTGSLPGFVDVIRNLNSPALLEDSDSVIRQAAGKRIIVFYGDETWKLPKHFVEYDGT 180
 QY 181 TSFFVSDVTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHISGNSPLIGOKLSEMD 240
 DB 181 TSFFVSDVTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHISGNSPLIGOKLSEMD 240
 QY 241 SVLMKIHTSLQSKERETPLNLLVLCGDHGMSETGSHGASSTEVNTPLILISSAFERKP 300
 DB 241 SVLMKIHTSLQSKERETPLNLLVLCGDHGMSETGSHGASSTEVNTPLILISSAFERKP 300
 QY 301 GDIRHPKHVQ 310
 DB 301 GDIRHPKHVQ 310
 RESULT 3
 AAB87595
 ID AAB87595 standard; protein; 310 AA.
 XX AC AAB87595;
 XX DT 15-MAY-2001 (first entry)
 XX DE Human PRO4405.
 XX KW Human; PRO protein; mapping.
 XX OS Homo sapiens.
 XX PN WO200116318-A2.
 XX PD 08-MAR-2001.
 XX PF 24-AUG-2000; 2000WO-US023328.
 XX PR 01-SEP-1999; 99WO-US020111.
 XX PR 15-SEP-1999; 99WO-US021090.
 XX PR 07-DEC-1999; 99US-0169495P.
 XX PR 09-DEC-1999; 99US-0170262P.
 XX PR 11-JAN-2000; 2000US-0175481P.
 XX PR 18-FEB-2000; 2000WO-US004341.
 XX PR 18-FEB-2000; 2000WO-US004342.
 XX PR 22-FEB-2000; 2000WO-US004414.
 XX PR 01-MAR-2000; 2000WO-US005601.
 XX PR 03-MAR-2000; 2000US-0187202P.
 XX PR 21-MAR-2000; 2000US-0191007P.
 XX PR 30-MAR-2000; 2000WO-US008439.
 XX PR 25-APR-2000; 2000US-0199397P.
 XX PR 22-MAY-2000; 2000WO-US014042.
 XX PR 05-JUN-2000; 2000US-0209832P.
 XX (GETH) GENENTECH INC.
 XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
 XX WPI; 2001-183260/18.
 DR N-PSDB; AAF92127.

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Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.

Claim 12; Fig 140; 278pp; English.

The present sequence is a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping

Sequence 310 AA;

Query Match 100.0%; Score 1617; DB 4; Length 310;
Best Local Similarity 100.0%; Pred. No. 4.6e-159;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLGSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPSAGASSNWTL 60
DB 1 MRLGSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPSAGASSNWTL 60
QY 61 PPPLFSKVVILIDALRDDDFVFGSKGVKFMPTTYTLVEKGASHFVAEAKPPTVTMPRIK 120
DB 61 PPPLFSKVVILIDALRDDDFVFGSKGVKFMPTTYTLVEKGASHFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGVDVIRNLNSPALLEDVIRQAKAGKRIVFYGDETWVKLPFKHFVEYDGT 180
DB 121 ALMTGSLPGVDVIRNLNSPALLEDVIRQAKAGKRIVFYGDETWVKLPFKHFVEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHGLDHLGHISGPNPLIGQKLSMD 240
DB 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHGLDHLGHISGPNPLIGQKLSMD 240
QY 241 SVLMKHTSLOSKERETPLNLAVLGDHGWSETSGHGSSTEEVNTPLILISSAFERXP 300
DB 241 SVLMKHTSLOSKERETPLNLAVLGDHGWSETSGHGSSTEEVNTPLILISSAFERXP 300
QY 301 GDIRHPKHVQ 310
DB 301 GDIRHPKHVQ 310

RESULT 4
AAU83650
XX AAU83650 standard; protein; 310 AA.
AC AAU83650;
XX
DT 08-MAY-2002 (first entry)
XX
XX Human PRO protein, Seq ID No 118.
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha.
XX Homo sapiens.
XX WO200208288-A2.
XX
XX 31-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US021066.
XX
XX 20-JUL-2000; 2000US-0219556P.
XX 25-JUL-2000; 2000US-0220585P.
XX 25-JUL-2000; 2000US-0220605P.

PR 25-JUL-2000; 2000US-0220607P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220638P.
PR 25-JUL-2000; 2000US-0220664P.
PR 25-JUL-2000; 2000US-0220666P.
PR 26-JUL-2000; 2000US-0220893P.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-AUG-2000; 2000US-0222445P.
PR 22-AUG-2000; 2000US-0227133P.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen WB, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
XX WPI; 2002-172001/22.
DR N-PSDB; ABK33594.
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful for treating a PRO related disorder and for diagnosing tumors such
XX as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
XX or liver tumor.
XX Claim 11; Fig 118; 359pp; English.
XX The invention relates to one hundred and twenty two nucleic acids
XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX agonists and antagonists are useful for treating a PRO related disorder.
XX The PRO polypeptides are useful for diagnosing tumors, especially lung
XX cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or
XX liver tumor. The PRO polypeptides are useful for stimulating the
XX proliferation of, or gene expression, in pericyte cells, for stimulating
XX the proliferation or differentiation of chondrocyte cells, for
XX stimulating the release of tumour necrosis factor-alpha from human blood,
XX for stimulating or inhibiting the proliferation of normal human dermal
XX fibroblast cells. The PRO polypeptide may also be used as molecular
XX weight markers and for tissue typing. The PRO nucleic acids have
XX applications in molecular biology, including use as hybridisation probes,
XX and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
XX protein sequences of the invention
XX SQ Sequence 310 AA;

Query Match 100.0%; Score 1617; DB 5; Length 310;
Best Local Similarity 100.0%; Pred. No. 4.6e-159;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLGSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPSAGASSNWTL 60
DB 1 MRLGSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPSAGASSNWTL 60
QY 61 PPPLFSKVVILIDALRDDDFVFGSKGVKFMPTTYTLVEKGASHFVAEAKPPTVTMPRIK 120
DB 61 PPPLFSKVVILIDALRDDDFVFGSKGVKFMPTTYTLVEKGASHFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGVDVIRNLNSPALLEDVIRQAKAGKRIVFYGDETWVKLPFKHFVEYDGT 180
DB 121 ALMTGSLPGVDVIRNLNSPALLEDVIRQAKAGKRIVFYGDETWVKLPFKHFVEYDGT 180

QY 181 TSFFVSDYTEVNNVTHRLDKVLRGWDWDLILHYLGLDHIHIGSPNSPLIGQKLSMD 240
DB 181 TSFFVSDYTEVNNVTHRLDKVLRGWDWDLILHYLGLDHIHIGSPNSPLIGQKLSMD 240
QY 241 SVLMKHTLSQSKERTPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
DB 241 SVLMKHTLSQSKERTPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
DB 301 GDIRHPKHVQ 310
RESULT 5
ABG95920
ID ABG95920 standard; protein; 310 AA.
XX
AC ABG95920;
DT 10-DEC-2002 (first entry)
DE Human secreted/transmembrane protein PRO4405.
XX
KW Human; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN US2002119130-A1.
XX
PD 29-AUG-2002.
XX
PF 06-DEC-2001; 2001US-00006867.
XX
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0083495P.
PR 15-MAY-1998; 98US-0085575P.
PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088029P.
PR 10-JUN-1998; 98US-0088030P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089552P.
PR 22-JUN-1998; 98US-0090246P.
PR 24-JUN-1998; 98US-0090444P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.

PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX (GETH) GENENTECH INC.
PA Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2002-731348/79.
XX N-PSDB; ABS74447.
PT New isolated secreted and transmembrane PRO polypeptide useful for
XX modulating biological activity of a cell, or for treating sports-related
XX joint problems, osteoarthritis or rheumatoid arthritis.
XX Claim 20; Fig 140; 399pp; English.
CC The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG95851-ABG9594 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a

CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence represents a novel secreted or transmembrane protein of the
CC invention
XX

SQ Sequence 310 AA;

Query Match 100.0%; Score 1617; DB 5; Length 310;
Best Local Similarity 100.0%; Pred. No. 4.6e-159; Mismatches 0; Gaps 0;
Matches 310; Conservative 0; Indels 0;
QY 1 MELSGTFTATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPEPSAGASSNWTTL 60
DB 1 MELSGTFTATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPEPSAGASSNWTTL 60
QY 61 PPLPSKVIVLIDALRDFVFGSKGVKPMPTTVTLVEKGASHSVFAEAKPPTVTMPRIK 120
DB 61 PPLPSKVIVLIDALRDFVFGSKGVKPMPTTVTLVEKGASHSVFAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLESVIRQAAGKRIIVFYGDETWWKLFPPHFVEYDGT 180
DB 121 ALMTGSLPGFVDVIRNLNSPALLESVIRQAAGKRIIVFYGDETWWKLFPPHFVEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILIHLYGLDHIHIGSPNSPLIGQKLSMD 240
DB 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILIHLYGLDHIHIGSPNSPLIGQKLSMD 240
QY 241 SVLMKHTSIQSKERTPLNLLVLCGDHGMSETSGHGSSTEEVNTPLILISSAFERKP 300
DB 241 SVLMKHTSIQSKERTPLNLLVLCGDHGMSETSGHGSSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
DB 301 GDIRHPKHVQ 310

RESULT 6
ABB84962
ID ABB84962 standard; protein; 310 AA.

AC ABB84962;

XX 16-MAY-2002 (first entry)

DE Human PRO4405 protein sequence SEQ ID NO:292.

XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW vulnary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping.

XX

OS Homo sapiens.

XX PN WO200200690-A2.

XX PD 03-JAN-2002.

XX PF 20-JUN-2001; 2001WO-US019692.

XX PR 23-JUN-2000; 2000US-0213637P.

XX PR 20-JUL-2000; 2000US-0219556P.

XX PR 25-JUL-2000; 2000US-0220624P.

XX PR 28-JUL-2000; 2000US-0220664P.

XX PR 02-AUG-2000; 2000WO-US020710.

XX PR 17-AUG-2000; 2000US-0222695P.

XX PR 23-AUG-2000; 2000US-00643657.

XX PR 24-AUG-2000; 2000WO-US023522.

XX PR 07-SEP-2000; 2000US-0230978P.

XX PR 18-SEP-2000; 2000US-00664610.

XX PR 18-SEP-2000; 2000US-00665350.

XX PR 24-OCT-2000; 2000US-0242922P.

XX PR 08-NOV-2000; 2000US-00709238.

XX PR 10-NOV-2000; 2000WO-US030952.

XX PR 01-DEC-2000; 2000WO-US030873.

XX PR 20-DEC-2000; 2000US-00747259.

XX PR 22-DEC-2000; 2000WO-US034956.

XX PR 28-FEB-2001; 2001US-00767609.

XX PR 28-FEB-2001; 2001US-00796498.

XX PR 28-FEB-2001; 2001WO-US006520.

XX PR 01-MAR-2001; 2001US-00066666.

XX PR 09-MAR-2001; 2001US-00802706.

XX PR 14-MAR-2001; 2001US-00808689.

XX PR 22-MAR-2001; 2001US-00816744.

XX PR 05-APR-2001; 2001US-00828366.

XX PR 10-MAY-2001; 2001US-00854208.

XX PR 25-MAY-2001; 2001US-00866028.

XX PR 25-MAY-2001; 2001US-00866034.

XX PR 30-MAY-2001; 2001WO-US017092.

XX PR 30-MAY-2001; 2001US-00870574.

XX PR 01-JUN-2001; 2001WO-US017443.

XX PR 01-JUN-2001; 2001WO-US017800.

XX (GETH) GENENTECH INC.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI; 2002-090516/12.

XX DR N-PSDB; ABL88217.

XX Claim 11; Fig 292; 565pp; English.

XX ABL88072 to ABL88258 encode the PRO proteins given in ABL884817 to

XX ABL885003. The PRO proteins and polynucleotides have cardiant, cytostatic,

XX antiangiogenic, hypotensive, vulnary and antiarteriosclerotic

XX activities, and can be used in gene therapy. The PRO polynucleotides,

XX proteins, agonists and antagonists are useful for treating or diagnosing

XX a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.

XX cardiac hypertrophy, trauma, cancer, age-related macular degeneration,

XX atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

XX angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound

XX healing. The PRO polynucleotides have applications in molecular biology,

XX including use as hybridisation probes, and in chromosome and gene

XX mapping. ABL88259 to ABL88267 represent primers and probes used in the

XX exemplification of the present invention

XX SQ Sequence 310 AA;

Query Match 100.0%; Score 1617; DB 5; Length 310;
Best Local Similarity 100.0%; Pred. No. 4.6e-159;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLSGTFTATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPSAGASSNWTL 60
DB 1 MRLSGTFTATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPSAGASSNWTL 60
QY 61 PPLFSKVIILDALRDDVFVSGSKGVKMPYTTLYVEKGASHSFVAEAKPPTVMPRIK 120
DB 61 PPLFSKVIILDALRDDVFVSGSKGVKMPYTTLYVEKGASHSFVAEAKPPTVMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAAAGKRIVFYGDETWVKLFPKHFEYDGT 180
DB 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAAAGKRIVFYGDETWVKLFPKHFEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHIGSPNSPLIGQKLSMD 240
DB 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHIGSPNSPLIGQKLSMD 240
QY 241 SVLMKHTLSQKERTPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERP 300
DB 241 SVLMKHTLSQKERTPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERP 300
QY 301 GDIRHPKHVQ 310
DB 301 GDIRHPKHVQ 310

RESULT 7
ABB95568
ID ABB95568 standard; protein; 310 AA.
AC ABB95568;
XX 19-JUL-2002 (first entry)
XX Human angiogenesis related protein PRO4405 SEQ ID NO: 292.
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
XX cardiac; cyostatic; antiangiogenic; hypotensive; vulnerary;
XX antiarteriosclerotic.
XX Homo sapiens.
XX WO200208284-A2.
XX 31-JAN-2002.
XX 09-JUL-2001; 2001WO-US021735.
XX 20-JUL-2000; 2000US-0219556P.
XX 25-JUL-2000; 2000US-0220624P.
XX 28-JUL-2000; 2000US-0220664P.
XX 28-JUL-2000; 2000WO-US020710.
XX 02-AUG-2000; 2000US-0222895P.
XX 17-AUG-2000; 2000US-00643657.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.
XX 07-SEP-2000; 2000US-0230978P.
XX 18-SEP-2000; 2000US-00664610.
XX 18-SEP-2000; 2000US-00665350.
XX 24-OCT-2000; 2000US-0242522P.
XX 08-NOV-2000; 2000US-00709238.
XX 08-NOV-2000; 2000WO-US030952.
XX 10-NOV-2000; 2000WO-US030873.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000US-00747259.
XX 20-DEC-2000; 2000WO-US034956.

22-JAN-2001; 2001US-00767609.
28-FEB-2001; 2001US-00796498.
28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US008666.
09-MAR-2001; 2001US-00802706.
14-MAR-2001; 2001US-00808689.
22-MAR-2001; 2001US-00816744.
05-APR-2001; 2001US-00828366.
10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001US-00866028.
25-MAY-2001; 2001US-00866034.
30-MAY-2001; 2001US-00870574.
30-MAY-2001; 2001WO-US017443.
01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
XX (GETH) GENENTECH INC.
PA (BAKE) BAKER K P.
PA (FERR) FERRARA N.
PA (GERB) GERBER H.
PA (GERR) GERRITSEN M E.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GURN) GURNEY A L.
PA (HILL) HILLAN K J.
PA (MARS) MARSTERS S A.
PA (PANJ) PAN J.
PA (PAON) PAONI N F.
PA (STEP) STEPHAN J F.
PA (WATA) WATANABE C K.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-171999/22.
DR N-PSDB; ABL95706.
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX Claim 11; Fig 292; 567pp; English.
PS The present invention provides the protein and coding sequences of human
XX PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention
XX Sequence 310 AA;
SQ Query Match 100.0%; Score 1617; DB 5; Length 310;
Best Local Similarity 100.0%; Pred. No. 4.6e-159;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLSGTFTATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPSAGASSNWTL 60
DB 1 MRLSGTFTATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPSAGASSNWTL 60
QY 61 PPLFSKVIILDALRDDVFVSGSKGVKMPYTTLYVEKGASHSFVAEAKPPTVMPRIK 120
DB 61 PPLFSKVIILDALRDDVFVSGSKGVKMPYTTLYVEKGASHSFVAEAKPPTVMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAAAGKRIVFYGDETWVKLFPKHFEYDGT 180

Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAAGKRIYFYGDETWWKLFPPKHFVEYDGT 180
 QY 181 TSFFVSDYTEVDNNVTRHLDKVLKGDWDILILHYGLDHDHIGHSNPSPLIGQKLSMD 240
 Db 181 TSFFVSDYTEVDNNVTRHLDKVLKGDWDILILHYGLDHDHIGHSNPSPLIGQKLSMD 240
 QY 241 SVLMKIHTSLOKRETPPLNLLVLCGDHGMSETSGHGASSTEEVNTPLILISSAFERKP 300
 Db 241 SVLMKIHTSLOKRETPPLNLLVLCGDHGMSETSGHGASSTEEVNTPLILISSAFERKP 300
 QY 301 GDIRHPKHVQ 310
 Db 301 GDIRHPKHVQ 310

RESULT 8
 ABU69112
 ID ABU69112 standard; protein; 310 AA.
 XX AC
 AC ABU69112;
 XX DT
 DT 02-JUN-2003 (first entry)
 XX DE
 DE Human PRO polypeptide #10.
 XX KW
 KW Human; secreted and transmembrane protein; bone disorder; obesity;
 KW cartilage disorder; sports injury; arthritis; diabetes mellitus;
 KW hypo-insulinaemia; obesity; hyper-insulinaemia; thalassaemia;
 KW haemoglobin-associated disorder; kidney disorder; Berger disease;
 KW mesangial cell function; nephropathy; Schonlein-Henoch purpura;
 KW celiac disease; dermatitis herpetiformis; Crohn's disease; anorectic;
 KW antiarthritic; antidiabetic; antianaemic; nephrotropic; antiinflammatory.
 XX OS
 OS Homo sapiens.
 XX PN
 PN US2003032061-A1.
 XX PD
 PD 13-FEB-2003.
 XX PF
 PF 26-DEC-2001; 2001US-00036214.
 XX PR
 PR 15-MAY-1998; 98US-0085579P.
 PR 15-DEC-1998; 98US-0112514P.
 PR 22-DEC-1998; 98US-0113300P.
 PR 23-DEC-1998; 98US-0113430P.
 PR 23-DEC-1998; 98US-0113605P.
 PR 23-DEC-1998; 98US-0113621P.
 PR 12-JAN-1999; 98US-0114140P.
 PR 12-JAN-1999; 98US-0115552P.
 PR 22-JAN-1999; 98US-0116843P.
 PR 23-MAR-1999; 98US-0125774P.
 PR 23-MAR-1999; 98US-0125778P.
 PR 24-MAR-1999; 98US-0125826P.
 PR 31-MAR-1999; 98US-0127035P.
 PR 05-APR-1999; 98US-0127706P.
 PR 13-APR-1999; 98US-0129122P.
 PR 21-APR-1999; 98US-0130359P.
 PR 27-APR-1999; 98US-0131270P.
 PR 27-APR-1999; 98US-0131272P.
 PR 27-APR-1999; 98US-0131291P.
 PR 04-MAY-1999; 98US-0132371P.
 PR 04-MAY-1999; 98US-0132379P.
 PR 04-MAY-1999; 98US-0132383P.
 PR 14-MAY-1999; 98US-0132383P.
 PR 25-MAY-1999; 98US-0135750P.
 PR 08-JUN-1999; 98US-0138466P.
 PR 20-JUL-1999; 98US-0144791P.
 PR 03-AUG-1999; 98US-0146970P.
 PR 29-OCT-1999; 98US-0162506P.
 PR 02-DEC-1999; 98US-028551.
 PR 22-DEC-1999; 98US-0303720.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.

PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023528.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 09-JUL-2001; 2001WO-US021066.
 PR 16-AUG-2001; 2001WO-US021735.
 XX XX
 XX (GETH) GENENTECH INC.
 XX
 XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
 PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
 XX
 XX WPI; 2003-341962/32.
 DR N-PSDB; ACA06159.
 XX
 XX Novel isolated PRO polypeptides e.g., PRO4334, PRO1122, PRO1889, PRO1890,
 PT PRO1887, PRO1785, PRO4353, useful for treating sports injuries,
 PT arthritis, diabetes, obesity, hyper- or hypo-insulinemia.
 XX
 XX Claim 12; Fig 20; 194pp; English.
 PS
 XX The present invention relates to the isolation of novel human PRO
 XX polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides and polynucleotides are useful in diagnosing or treating
 CC various bone and/or cartilage disorders (e.g. sports injuries,
 CC arthritis), various insulin deficient states (e.g. diabetes mellitus,
 CC hypo-insulinaemia), obesity, hyper-insulinaemia, haemoglobin-associated
 CC disorders (e.g. thalassaemias), kidney disorders associated with
 CC decreased mesangial cell function (e.g. Berger disease), or other
 CC nephropathies associated with Schonlein-Henoch purpura, celiac disease,
 CC dermatitis herpetiformis or Crohn's disease. The PRO polynucleotide
 CC sequences may be used as hybridisation probes in chromosome and gene
 CC mapping, or in generating antisense RNA and DNA. They are also useful in
 CC preparing PRO polypeptides, in assays to identify other proteins or
 CC molecules involved in binding reaction, to generate transgenic animals or
 CC knockout animals, which in turn are useful in the development and
 CC screening of therapeutically useful reagents, for chromosome
 CC identification, and tissue typing. The PRO polypeptides and nucleic acid
 CC molecules are also useful in gene therapy, and as molecular weight
 CC markers for protein electrophoresis purposes. Anti-PRO antibodies may be
 CC used in diagnostic assays for PRO polypeptides, or for the affinity
 CC purification of the polypeptides from recombinant cell culture or natural
 CC sources. ABU69103-ABU69125 represent the human PRO polypeptides of the
 CC invention
 XX
 XX Sequence 310 AA;
 SQ

Query Match 100.0%; Score 1617; DB 6; Length 310;
 Best Local Similarity 100.0%; Pred. No. 4.6e-159;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGSGTATCCVATEVLGIAVFLRGFPFAPVRSARAHEGAEPPAPEPSAGASNWTTL 60
 Db 1 MELGSGTATCCVATEVLGIAVFLRGFPFAPVRSARAHEGAEPPAPEPSAGASNWTTL 60
 QY 61 PPPLFSKVVIVLIDALRDDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPTVTMPRIK 120
 Db 61 PPPLFSKVVIVLIDALRDDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPTVTMPRIK 120
 QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAAGKRIYFYGDETWWKLFPPKHFVEYDGT 180
 Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAAGKRIYFYGDETWWKLFPPKHFVEYDGT 180
 QY 181 TSFFVSDYTEVDNNVTRHLDKVLKGDWDILILHYGLDHDHIGHSNPSPLIGQKLSMD 240
 Db 181 TSFFVSDYTEVDNNVTRHLDKVLKGDWDILILHYGLDHDHIGHSNPSPLIGQKLSMD 240

QY 241 SVLMKIHTSLOSKERETPLNLLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
 DB 241 SVLMKIHTSLOSKERETPLNLLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
 QY 301 GDIRHPKHVQ 310
 DB 301 GDIRHPKHVQ 310

RESULT 9
 ID ABU80797 standard; protein; 310 AA.
 XX ABU80797;
 XX 23-JUN-2003 (first entry)
 XX Human PRO polypeptide #59.
 XX Human; PRO polypeptide; secreted and transmembrane protein;
 XX anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
 XX Homo sapiens.
 XX US2003036635-A1.
 XX 20-FEB-2003.
 XX 28-AUG-2002; 2002US-00230163.
 XX 25-JUL-2000; 2000US-0220638P.
 XX 01-JUN-2001; 2001WO-US017800.
 XX 29-JUN-2001; 2001WO-US021066.
 XX 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-342045/32.
 XX N-PSDB; ACA66899.
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 XX useful for the manufacture of a medicament for diagnosing or treating
 XX tumor.
 XX Claim 11; Fig 118; 314pp; English.
 XX The present invention relates to the isolation of novel human PRO
 XX polypeptides, and the polynucleotide sequences encoding them. The PRO
 XX polypeptides are secreted and transmembrane proteins. The PRO
 XX polypeptides and polynucleotides are useful for preparing a medicament
 XX useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
 XX useful in diagnostic assays for PRO, by detecting its expression in
 XX specific cells, tissues or serum, and for affinity purification of PRO
 XX from recombinant cell culture or natural sources. ABU80739-ABU80860
 XX represent the human PRO polypeptides of the invention. Note: The sequence
 XX data for this patent was obtained in electronic format directly from the
 XX USPTO web site at seqdata.uspto.gov/psipdsIDEntry.html
 XX Sequence 310 AA;
 XX Query Match 100.0%; Score 1617; DB 6; Length 310;
 XX Best Local Similarity 100.0%; Pred. NO. 4.6e-159;
 XX Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIGSGTFTATCCVAIEVLGIAVFLRGFFPAPVRSARAEHGAEPAPSPSAGASSNWTTL 60
 DB 1 MRIGSGTFTATCCVAIEVLGIAVFLRGFFPAPVRSARAEHGAEPAPSPSAGASSNWTTL 60
 QY 61 PPPLFSKVVIVLIDALRDDDFVFGSKGVKMPYTTYLVKGGASHSFVAEAKPPTVTMPRIK 120

DB 61 PPPLFSKVVIVLIDALRDDDFVFGSKGVKMPYTTYLVKGGASHSFVAEAKPPTVTMPRIK 120
 QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGRIIVFYGDETWWKLPFKHFVEYDGT 180
 DB 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGRIIVFYGDETWWKLPFKHFVEYDGT 180
 QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWLILHLGLDHIHIGSPNSPLIGCKLSEMD 240
 DB 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWLILHLGLDHIHIGSPNSPLIGCKLSEMD 240
 QY 241 SVLMKIHTSLOSKERETPLNLLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
 DB 241 SVLMKIHTSLOSKERETPLNLLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
 QY 301 GDIRHPKHVQ 310
 DB 301 GDIRHPKHVQ 310

RESULT 10
 ID ABO33763 standard; protein; 310 AA.
 XX ABO33763;
 XX 17-SEP-2003 (first entry)
 XX Novel human secreted and transmembrane protein PRO4405.
 XX Human; secreted and transmembrane protein; PRO; cytostatic;
 XX antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
 XX chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
 XX pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;
 XX colon tumour; breast tumour; prostate tumour; rectal tumour;
 XX liver tumour; bone disorder; cartilage disorder; sports injury;
 XX arthritis; wound.
 XX Homo sapiens.
 XX US2003045687-A1.
 XX 06-MAR-2003.
 XX 12-AUG-2002; 2002US-00218631.
 XX 01-JUN-2001; 2001WO-US017800.
 XX 29-JUN-2001; 2001WO-US021066.
 XX 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-512315/48.
 XX N-PSDB; ACD66651.
 XX New genes, and its encoded secreted and transmembrane polypeptides,
 XX useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
 XX pericyte proliferation, especially for treating lung tumors, arthritis or
 XX wounds in a mammal.
 XX Claim 11; Fig 118; 314pp; English.
 XX The invention describes an isolated nucleic acid molecule comprising a
 XX sequence with at least 80% identity to: (a) a nucleotide encoding any of
 XX 122 PRO (secreted and transmembrane) polypeptides whose sequences are
 XX fully defined in the specification; or (b) any of 122 nucleotide
 XX sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
 XX specification; or the full length coding sequence of any these 122
 XX nucleotide sequences. The PRO polypeptides or polynucleotides are useful
 XX as pharmaceuticals, diagnostics, biosensors or bioreactors. these are

CC particularly useful for detecting tumours (e.g. lung tumour, colon
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC in a mammal, for stimulating the release of TNP-alpha from human blood,
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells, for stimulating proliferation of pericyte cells, or for modulating
CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
CC polypeptide is also useful for treating tumours or various bone and/or
CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide

XX Sequence 310 AA;

Query Match 100.0%; Score 1617; DB 6; Length 310;
Best Local Similarity 100.0%; Pred. No. 4.6e-159;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLGSGTATCCCAIEVLGIAVFLRGFFPAPVRSARAEGHGAEPPEPSAGASSNWTL 60
DB 1 MRLGSGTATCCCAIEVLGIAVFLRGFFPAPVRSARAEGHGAEPPEPSAGASSNWTL 60
QY 61 PPLFSKVVILIDALRDDDFVFGSKGVKMPYTYLVEKGASHSFVAEAKPTVTMPRIK 120
DB 61 PPLFSKVVILIDALRDDDFVFGSKGVKMPYTYLVEKGASHSFVAEAKPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVSVIRQAAGKRIIVFYGDETWVKLPFKHFVEYDGT 180
DB 121 ALMTGSLPGFVDVIRNLNSPALLEDVSVIRQAAGKRIIVFYGDETWVKLPFKHFVEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHISGPNPLIGQKLSMD 240
DB 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHISGPNPLIGQKLSMD 240
QY 241 SVLMKIHTSLOSKEKETPLPNIIVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
DB 241 SVLMKIHTSLOSKEKETPLPNIIVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
DB 301 GDIRHPKHVQ 310

RESULT 11
ABU90945
ID ABU90945 standard; protein; 310 AA.
AC ABU90945;
XX
XX 11-JUL-2003 (first entry)
DE Novel human secreted and transmembrane protein PRO4405.
XX Human; secreted and transmembrane protein; PRO; antibody therapy;
XX pharmaceutical; diagnostic; biosensor; bioreactor.
XX Homo sapiens.
OS
XX US2003018173-A1.
PN
XX 23-JAN-2003.
XX
XX 01-MAY-2002; 2002US-00063515.
XX
XX 06-DEC-2001; 2001US-00006867.
XX
XX (GETH) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2003-401702/38.
DR N-PSDB; ACA91233.
XX New antibody useful for identifying PRO polypeptides, for affinity
PT purification of PRO polypeptides, and for preparing a medicament for
PT diagnosing or treating conditions responsive to the antibody or PRO
PT polypeptide.
XX Disclosure; Fig 140; 345pp; English.

XX The invention describes an antibody that specifically binds to a PRO
XX polypeptide having a fully defined amino acid sequence given in the
CC specification. The antibody is useful in identifying PRO polypeptides
CC useful for various industrial applications, including pharmaceuticals,
CC diagnostics, biosensors and bioreactors. The antibody is also used for
CC affinity purification of PRO polypeptides from recombinant cell culture
CC or natural sources. The antibody, PRO polypeptide, or its agonists or
CC antagonists, may be used for preparing a medicament for diagnosing or
CC treating a condition responsive to the antibody, PRO polypeptide, or its
CC agonists or antagonists. This is the amino acid sequence of a novel human
XX secreted and transmembrane PRO polypeptide

XX Sequence 310 AA;

Query Match 100.0%; Score 1617; DB 6; Length 310;
Best Local Similarity 100.0%; Pred. No. 4.6e-159;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLGSGTATCCCAIEVLGIAVFLRGFFPAPVRSARAEGHGAEPPEPSAGASSNWTL 60
DB 1 MRLGSGTATCCCAIEVLGIAVFLRGFFPAPVRSARAEGHGAEPPEPSAGASSNWTL 60
QY 61 PPLFSKVVILIDALRDDDFVFGSKGVKMPYTYLVEKGASHSFVAEAKPTVTMPRIK 120
DB 61 PPLFSKVVILIDALRDDDFVFGSKGVKMPYTYLVEKGASHSFVAEAKPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVSVIRQAAGKRIIVFYGDETWVKLPFKHFVEYDGT 180
DB 121 ALMTGSLPGFVDVIRNLNSPALLEDVSVIRQAAGKRIIVFYGDETWVKLPFKHFVEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHISGPNPLIGQKLSMD 240
DB 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHISGPNPLIGQKLSMD 240
QY 241 SVLMKIHTSLOSKEKETPLPNIIVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
DB 241 SVLMKIHTSLOSKEKETPLPNIIVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
DB 301 GDIRHPKHVQ 310

RESULT 12
ABO34004
ID ABO34004 standard; protein; 310 AA.
XX ABO34004;
XX
XX 18-SEP-2003 (first entry)
XX Human secreted/transmembrane protein PRO4405.
XX Human; secreted/transmembrane protein; PRO; tumour; cancer; cytostatic.
XX Homo sapiens.
XX US2003009013-A1.
XX

PD 09-JAN-2003.
XX 01-MAY-2002; 2002US-00063519.
XX 30-DEC-1998; 98KE-00062142.
XX 08-MAR-1999; 99WO-US005028.
XX 14-MAY-1999; 99WO-US011832.
XX 14-MAY-1999; 99WO-US010733.
XX 25-AUG-1999; 99US-00380137.
XX 25-AUG-1999; 99US-00380138.
XX 25-AUG-1999; 99US-00380139.
XX 25-AUG-1999; 99US-00380142.
XX 15-SEP-1999; 99US-00397342.
XX 18-OCT-1999; 99US-00403297.
XX 12-NOV-1999; 99US-00423844.
XX 30-DEC-1999; 99WO-US031274.
XX 18-FEB-2000; 2000WO-US004341.
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005841.
XX 21-MAR-2000; 2000WO-US007532.
XX 22-MAY-2000; 2000WO-US014042.
XX 02-JUN-2000; 2000WO-US015264.
XX 22-AUG-2000; 2000WO-US023328.
XX 18-SEP-2000; 2000US-00664610.
XX 18-SEP-2000; 2000US-00665350.
XX 08-NOV-2000; 2000US-00709238.
XX 10-NOV-2000; 2000WO-US030873.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000US-00747259.
XX 20-DEC-2000; 2000WO-US034956.
XX 28-FEB-2001; 2001WO-US006520.
XX 22-MAR-2001; 2001US-00816744.
XX 10-MAY-2001; 2001US-00854208.
XX 10-MAY-2001; 2001US-00854280.
XX 30-MAY-2001; 2001US-00870574.
XX 01-JUN-2001; 2001WO-US017800.
XX 05-JUN-2001; 2001US-00874503.
XX 29-JUN-2001; 2001US-00869599.
XX 18-JUL-2001; 2001US-00908827.
XX 08-DEC-2001; 2001US-00008667.
XX (GETH) GENENTECH INC.
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2003-447384/42.
XX N-PSDB; ACD91610.
XX
XX New isolated antibody specifically binding a PRO polypeptide, useful for
XX the preparation of a medicament for treating disorders with the aberrant
XX expression or activity of the PRO polypeptide, such as tumor conditions
XX and cancer.
XX
XX Disclosure; Fig 140; 223pp; English.
XX
XX The invention relates to an antibody that binds to a secreted or
XX transmembrane protein designated PRO1446 appearing as AB033941. The
XX protein is one of 84 PRO polypeptides which (along with their encoding
XX nucleic acids) are disclosed in the specification. The methods and
XX compositions of the present invention are useful for the preparation of a
XX medicament for the treatment of disorders associated with the aberrant
XX expression or activity of the PRO polypeptide, such as tumour conditions
XX and cancer. They can also be used to generate transgenic or knockout
XX animals useful in the development and screening of therapeutically useful
XX reagents. The PRO polypeptides and encoding nucleic acids can be used as
XX molecular weight markers for protein electrophoresis, chromosome
XX identification and tissue typing. The antibodies may be used in various
XX diagnostic, competitive binding and/or immunoprecipitation assays. The
XX present sequence represents a PRO polypeptide
XX Sequence 310 AA;

Query Match 100.0%; Score 1617; DB 6; Length 310;
Best Local Similarity 100.0%; Pred. No. 4.6e-159;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLGSGTATCCCAIEVLGIAVFLRGFPAPVSSSARAEGHGAEPAPESAGASSNWTL 60
DB 1 MRLGSGTATCCCAIEVLGIAVFLRGFPAPVSSSARAEGHGAEPAPESAGASSNWTL 60
QY 61 PPPLFSKVIIVLIDALRDDVFVSGKGVKMPYTTILVEKGCASHSFVAEAKPPTVTMPRIK 120
DB 61 PPPLFSKVIIVLIDALRDDVFVSGKGVKMPYTTILVEKGCASHSFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLSPALLEDVSIRQAAGKRIIVFYGDETWVKLPFKHFVEYDGT 180
DB 121 ALMTGSLPGFVDVIRNLSPALLEDVSIRQAAGKRIIVFYGDETWVKLPFKHFVEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHLYGLDHIHISGPNPLIGOKLSEMD 240
DB 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHLYGLDHIHISGPNPLIGOKLSEMD 240
QY 241 SVLMKIHTSLQSKERETPLNLLVLCGDHGMSTGSHGASSTBEVNTPLILISSAFERKP 300
DB 241 SVLMKIHTSLQSKERETPLNLLVLCGDHGMSTGSHGASSTBEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
DB 301 GDIRHPKHVQ 310
RESULT 13
AB019428
ID AB019428 standard; protein; 310 AA.
XX AC AB019428;
XX DT 27-AUG-2003 (first entry)
XX DE Human secreted / transmembrane polypeptide PRO4405.
XX KW Human; gene therapy; diabetes; obesity; hypoinsulinaemia.
XX OS Homo sapiens.
XX PN US2003027249-A1.
XX PD 06-FEB-2003.
XX PF 16-AUG-2001; 2001US-00931836.
XX 15-MAY-1998; 98US-0085579P.
XX 15-DEC-1998; 98US-0112514P.
XX 22-DEC-1998; 98US-0113300P.
XX 23-DEC-1998; 98US-0113430P.
XX 23-DEC-1998; 98US-0113605P.
XX 23-DEC-1998; 98US-0113621P.
XX 23-DEC-1998; 98US-0114140P.
XX 12-JAN-1999; 99US-0115552P.
XX 22-JAN-1999; 99US-0116843P.
XX 23-MAR-1999; 99US-0125774P.
XX 23-MAR-1999; 99US-0125778P.
XX 31-MAR-1999; 99US-0127035P.
XX 05-APR-1999; 99US-0129122P.
XX 13-APR-1999; 99US-0130359P.
XX 21-APR-1999; 99US-0131270P.
XX 27-APR-1999; 99US-0131272P.
XX 27-APR-1999; 99US-0131291P.
XX 04-MAY-1999; 99US-0132371P.
XX 04-MAY-1999; 99US-0132379P.
XX 14-MAY-1999; 99US-0132383P.
XX 14-MAY-1999; 99US-00311832.

PR 14-MAY-1999; 99WO-US010733.
PR 25-MAY-1999; 99US-0135750P.
PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 25-AUG-1999; 99US-00380142.
PR 29-OCT-1999; 99US-0162508P.
PR 02-DEC-1999; 99WO-US028551.
PR 22-DEC-1999; 99WO-US030720.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001US-00869599.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
XX (GETH) GENENTECH INC.
XX
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-492030/46.
XX N-PSDB; ACD28828.
XX
XX New isolated, secreted and transmembrane PRO polypeptides and encoding
PT nucleic acids, useful for the diagnosis and treatment of disorders such
PT as diabetes, obesity and/or hypoinulinemia.
XX
XX Claim 12; Fig 20; 196pp; English.
XX
XX The invention relates to a new isolated nucleic acid which encodes a PRO
CC polypeptide. The methods and compositions of the present invention are
CC useful for the diagnosis and treatment of disorders associated with the
CC PRO polypeptides, such as diabetes, obesity and hypoinulinemia. The
CC present sequence represents the amino acid sequence of a human secreted
CC and transmembrane PRO polypeptide
XX
XX Sequence 310 AA;
Query Match 100.0%; Score 1617; DB 6; Length 310;
Best Local Similarity 100.0%; Pred. No. 4.6e-159; Indels 0; Gaps 0;
Matches 310; Conservative 0; Mismatches 0;
QY 1 MRLSGSTFATCCVAIEVLGIAVFLRGFFPAPVRESSARAEGHAPPPAPPSAGASNWTTL 60
DB 1 MRLSGSTFATCCVAIEVLGIAVFLRGFFPAPVRESSARAEGHAPPPAPPSAGASNWTTL 60
QY 61 PPLFSGKVVILDALRDDVFGSGKVGKFMPTTYLLVEKGASHSFVAEAKPPTVMPRIK 120
DB 61 PPLFSGKVVILDALRDDVFGSGKVGKFMPTTYLLVEKGASHSFVAEAKPPTVMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSFALLESVDVIRQAKAGKRIYFGDETWVKLFPKHFVEYDGT 180
DB 121 ALMTGSLPGFVDVIRNLNSFALLESVDVIRQAKAGKRIYFGDETWVKLFPKHFVEYDGT 180
QY 181 TSFVSDYTEVDNNVTNTHLKDVKLKGWDVILILHGLDHLGHISGPNPLICQKLSMD 240
DB 181 TSFVSDYTEVDNNVTNTHLKDVKLKGWDVILILHGLDHLGHISGPNPLICQKLSMD 240

QY 241 SVLMKHTSLOSKERTPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAPERKP 300
DB 241 SVLMKHTSLOSKERTPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAPERKP 300
QY 301 GDIRHPKHVQ 310
DB 301 GDIRHPKHVQ 310
RESULT 14
ABU72021
ID ABU72021 standard; protein; 310 AA.
XX AC ABU72021;
XX 11-JUN-2003 (first entry)
XX Novel human secreted and transmembrane protein PRO4405.
XX Human; secreted and transmembrane polypeptide; chromosome mapping;
KW gene mapping; transgenic animal; knockout animal;
KW therapeutic agent screening; chromosome identification; tissue typing;
KW gene therapy.
XX
XX Homo sapiens.
OS
XX US2003018183-A1.
XX 23-JAN-2003.
PD
XX 01-MAY-2002; 2002US-00063512.
XX 06-DEC-2001; 2001US-00006867.
XX (GETH) GENENTECH INC.
XX
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2003-330984/31.
XX N-PSDB; ACA60432.
XX
XX New secreted and transmembrane PRO polypeptides and nucleic acid
PT molecules encoding the polypeptides, useful in gene therapy or preparing
PT a medicament for treating a condition that is responsive to the PRO
PT polypeptide or antibody.
XX
XX Disclosure; Fig 140; 409pp; English.
XX
XX The invention describes novel isolated PRO polypeptides. The PRO
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC for treating a condition that is responsive to the PRO polypeptide or
CC antibody. The PRO nucleotide sequences may be used as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA and
CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in
CC assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. This is the amino acid sequence of a novel
CC human secreted and transmembrane PRO polypeptide
XX
XX Sequence 310 AA;

Query Match 100.0%; Score 1617; DB 6; Length 310;
Best Local Similarity 100.0%; Pred. No. 4.6e-159;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLGSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPBPSAGASSNWTL 60
Db 1 MRLGSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPBPSAGASSNWTL 60
QY 61 PPLPFSKVIWILIDALRDDDFVFGSGKGVKMPYTTLYLVEKGASHSFVAEAKPPTVTMPRIK 120
Db 61 PPLPFSKVIWILIDALRDDDFVFGSGKGVKMPYTTLYLVEKGASHSFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGRIIVFYGDETWWKLPFKHFVEYDGT 180
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGRIIVFYGDETWWKLPFKHFVEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHIGSPNSPLIGQKLSMD 240
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHIGSPNSPLIGQKLSMD 240
QY 241 SVLMKIHTSLQSKERTPLPNLLVLCGDHGMSETSGHGASSTEEVNTPLILISSAFERKP 300
Db 241 SVLMKIHTSLQSKERTPLPNLLVLCGDHGMSETSGHGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
Db 301 GDIRHPKHVQ 310

RESULT 15
ABU71575
ID ABU71575 standard; protein; 310 AA.

XX AC ABU71575;
XX DT 10-JUN-2003 (first entry)
XX DE Human secreted polypeptide PRO4405.
XX KW Human; gene therapy; tumour; cancer.
XX OS Homo sapiens.
XX PN US2003013855-A1.
XX PD 16-JAN-2003.
XX PF 03-MAY-2002; 2002US-00063616.
XX PR 30-DEC-1998; 98KR-00062142.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 14-MAY-1999; 99US-00311832.
XX PR 14-MAY-1999; 99WO-US010733.
XX PR 25-AUG-1999; 99US-00380137.
XX PR 25-AUG-1999; 99US-00380138.
XX PR 25-AUG-1999; 99US-00380139.
XX PR 25-AUG-1999; 99US-00380142.
XX PR 15-SEP-1999; 99US-00397342.
XX PR 18-OCT-1999; 99US-00403297.
XX PR 12-NOV-1999; 99US-00423844.
XX PR 30-DEC-1999; 99WO-US031274.
XX PR 18-FEB-2000; 2000WO-US004341.
XX PR 01-MAR-2000; 2000WO-US005601.
XX PR 02-MAR-2000; 2000WO-US005841.
XX PR 21-MAR-2000; 2000WO-US007532.
XX PR 22-MAY-2000; 2000WO-US014042.
XX PR 02-JUN-2000; 2000WO-US015264.
XX PR 22-AUG-2000; 2000WO-00644848.
XX PR 24-AUG-2000; 2000WO-US023328.
XX PR 18-SEP-2000; 2000US-0064610.
XX PR 18-SEP-2000; 2000US-00665350.
XX PR 08-NOV-2000; 2000US-00709238.
XX PR 01-DEC-2000; 2000WO-US030873.
XX PR 10-NOV-2000; 2000WO-US032678.
XX PR 20-DEC-2000; 2000US-00747259.
XX PR 20-DEC-2000; 2000WO-US034956.
XX PR 28-FEB-2001; 2001WO-US0006520.

PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 30-MAY-2001; 2001US-00854280.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00008867.
PA (GETH) GENENTECH INC.
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2003-330485/31.
DR N-PSDB; ACAS9879.
XX
XX New isolated antibody specifically binding a PRO polypeptide, useful for
PT the preparation of a medicament for treating disorders with the aberrant
PT expression or activity of the PRO polypeptide, such as tumor conditions
PT and cancer.
XX
XX Example 16; Page 212-213; 406pp; English.

XX The invention relates to an antibody that binds to a polypeptide with a
CC fully defined sequence given in the specification. The methods and
CC compositions (containing antibodies that specifically bind a PRO
CC polypeptide) of the present invention are useful for the preparation of a
CC medicament for the treatment of disorders associated with the aberrant
CC expression or activity of the PRO polypeptide, such as tumor conditions
CC and cancer. They can also be used to generate transgenic or knockout
CC animals useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
CC molecular weight markers for protein electrophoresis, chromosome
CC identification and tissue typing. The PRO polypeptides are useful to
CC induce angiogenesis e.g wound healing; in the treatment of sports-related
CC joint problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The
CC antibodies may be used in various diagnostic, competitive binding and/or
CC immunoprecipitation assays. The present sequence represents the amino
CC acid sequence of a PRO polypeptide of the invention

XX Sequence 310 AA;

Query Match 100.0%; Score 1617; DB 6; Length 310;
Best Local Similarity 100.0%; Pred. No. 4.6e-159;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLGSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPBPSAGASSNWTL 60
Db 1 MRLGSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPBPSAGASSNWTL 60
QY 61 PPLPFSKVIWILIDALRDDDFVFGSGKGVKMPYTTLYLVEKGASHSFVAEAKPPTVTMPRIK 120
Db 61 PPLPFSKVIWILIDALRDDDFVFGSGKGVKMPYTTLYLVEKGASHSFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGRIIVFYGDETWWKLPFKHFVEYDGT 180
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGRIIVFYGDETWWKLPFKHFVEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHIGSPNSPLIGQKLSMD 240
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHIGSPNSPLIGQKLSMD 240
QY 241 SVLMKIHTSLQSKERTPLPNLLVLCGDHGMSETSGHGASSTEEVNTPLILISSAFERKP 300
Db 241 SVLMKIHTSLQSKERTPLPNLLVLCGDHGMSETSGHGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
Db 301 GDIRHPKHVQ 310

89	1617	100.0	310	14	US-10-219-065-118	Sequence 118, App	162	100.0	310	14	US-10-063-736-140	Sequence 140, App
90	1617	100.0	310	14	US-10-219-071-118	Sequence 118, App	163	100.0	310	14	US-10-063-742-140	Sequence 140, App
91	1617	100.0	310	14	US-10-219-074-118	Sequence 118, App	164	100.0	310	14	US-10-063-743-140	Sequence 140, App
92	1617	100.0	310	14	US-10-219-077-118	Sequence 118, App	165	100.0	310	14	US-10-063-744-140	Sequence 140, App
93	1617	100.0	310	14	US-10-219-465-118	Sequence 118, App	166	100.0	310	14	US-10-063-565-140	Sequence 140, App
94	1617	100.0	310	14	US-10-219-467-118	Sequence 118, App	167	100.0	310	14	US-10-063-577-140	Sequence 140, App
95	1617	100.0	310	14	US-10-219-469-118	Sequence 118, App	168	100.0	310	14	US-10-063-591-140	Sequence 140, App
96	1617	100.0	310	14	US-10-219-471-118	Sequence 118, App	169	100.0	310	14	US-10-063-610-140	Sequence 140, App
97	1617	100.0	310	14	US-10-219-476-118	Sequence 118, App	170	100.0	310	14	US-10-063-673-140	Sequence 140, App
98	1617	100.0	310	14	US-10-219-476-118	Sequence 118, App	171	100.0	310	14	US-10-063-710-140	Sequence 140, App
99	1617	100.0	310	14	US-10-219-482-118	Sequence 118, App	172	100.0	310	14	US-10-063-711-140	Sequence 140, App
100	1617	100.0	310	14	US-10-227-874-118	Sequence 118, App	173	100.0	310	14	US-10-063-712-140	Sequence 140, App
101	1617	100.0	310	14	US-10-227-876-118	Sequence 118, App	174	100.0	310	14	US-10-063-714-140	Sequence 140, App
102	1617	100.0	310	14	US-10-227-878-118	Sequence 118, App	175	100.0	310	14	US-10-063-715-140	Sequence 140, App
103	1617	100.0	310	14	US-10-228-974-118	Sequence 118, App	176	100.0	310	14	US-10-063-716-140	Sequence 140, App
104	1617	100.0	310	14	US-10-230-024-118	Sequence 118, App	177	100.0	310	14	US-10-063-717-140	Sequence 140, App
105	1617	100.0	310	14	US-10-230-113-118	Sequence 118, App	178	100.0	310	14	US-10-063-720-140	Sequence 140, App
106	1617	100.0	310	14	US-10-230-183-118	Sequence 118, App	179	100.0	310	14	US-10-063-722-140	Sequence 140, App
107	1617	100.0	310	14	US-10-230-234-118	Sequence 118, App	180	100.0	310	14	US-10-063-726-140	Sequence 140, App
108	1617	100.0	310	14	US-10-230-306-118	Sequence 118, App	181	100.0	310	14	US-10-063-728-140	Sequence 140, App
109	1617	100.0	310	14	US-10-230-426-118	Sequence 118, App	182	100.0	310	14	US-10-063-731-140	Sequence 140, App
110	1617	100.0	310	14	US-10-230-427-118	Sequence 118, App	183	100.0	310	14	US-10-063-732-140	Sequence 140, App
111	1617	100.0	310	14	US-10-230-433-118	Sequence 118, App	184	100.0	310	14	US-10-063-523-140	Sequence 140, App
112	1617	100.0	310	14	US-10-230-435-118	Sequence 118, App	185	100.0	310	14	US-10-063-527-140	Sequence 140, App
113	1617	100.0	310	14	US-10-230-438-118	Sequence 118, App	186	100.0	310	14	US-10-063-579-140	Sequence 140, App
114	1617	100.0	310	14	US-10-232-222-118	Sequence 118, App	187	100.0	310	14	US-10-063-581-140	Sequence 140, App
115	1617	100.0	310	14	US-10-232-084-292	Sequence 232, App	188	100.0	310	14	US-10-063-583-140	Sequence 140, App
116	1617	100.0	310	14	US-10-232-088-292	Sequence 232, App	189	100.0	310	14	US-10-063-589-140	Sequence 140, App
117	1617	100.0	310	14	US-10-232-090-292	Sequence 232, App	190	100.0	310	14	US-10-063-593-140	Sequence 140, App
118	1617	100.0	310	14	US-10-219-070-118	Sequence 118, App	191	100.0	310	14	US-10-063-596-140	Sequence 140, App
119	1617	100.0	310	14	US-10-219-072-118	Sequence 118, App	192	100.0	310	14	US-10-063-600-140	Sequence 140, App
120	1617	100.0	310	14	US-10-219-527-118	Sequence 118, App	193	100.0	310	14	US-10-063-604-140	Sequence 140, App
121	1617	100.0	310	14	US-10-227-877-118	Sequence 118, App	194	100.0	310	14	US-10-063-607-140	Sequence 140, App
122	1617	100.0	310	14	US-10-063-560-140	Sequence 140, App	195	100.0	310	14	US-10-063-612-140	Sequence 140, App
123	1617	100.0	310	14	US-10-232-087-292	Sequence 232, App	196	100.0	310	14	US-10-063-615-140	Sequence 140, App
124	1617	100.0	310	14	US-10-063-557-140	Sequence 140, App	197	100.0	310	14	US-10-063-640-140	Sequence 140, App
125	1617	100.0	310	14	US-10-063-585-140	Sequence 140, App	198	100.0	310	14	US-10-063-642-140	Sequence 140, App
126	1617	100.0	310	14	US-10-232-083-292	Sequence 232, App	199	100.0	310	14	US-10-063-644-140	Sequence 140, App
127	1617	100.0	310	14	US-10-216-166-118	Sequence 118, App	200	100.0	310	14	US-10-063-649-140	Sequence 140, App
128	1617	100.0	310	14	US-10-218-612-118	Sequence 118, App	201	100.0	310	14	US-10-063-650-140	Sequence 140, App
129	1617	100.0	310	14	US-10-232-089-292	Sequence 232, App	202	100.0	310	14	US-10-063-652-140	Sequence 140, App
130	1617	100.0	310	14	US-10-063-588-140	Sequence 140, App	203	100.0	310	14	US-10-063-654-140	Sequence 140, App
131	1617	100.0	310	14	US-10-035-977-45	Sequence 45, App1	204	100.0	310	14	US-10-063-659-140	Sequence 140, App
132	1617	100.0	310	14	US-10-063-735-140	Sequence 140, App	205	100.0	310	14	US-10-063-661-140	Sequence 140, App
133	1617	100.0	310	14	US-10-216-163-118	Sequence 118, App	206	100.0	310	14	US-10-063-528-140	Sequence 140, App
134	1617	100.0	310	14	US-10-063-526-140	Sequence 140, App	207	100.0	310	14	US-10-063-540-140	Sequence 140, App
135	1617	100.0	310	14	US-10-063-596-140	Sequence 140, App	208	100.0	310	14	US-10-063-568-140	Sequence 140, App
136	1617	100.0	310	14	US-10-063-546-140	Sequence 140, App	209	100.0	310	14	US-10-063-570-140	Sequence 140, App
137	1617	100.0	310	14	US-10-063-564-140	Sequence 140, App	210	100.0	310	14	US-10-063-582-140	Sequence 140, App
138	1617	100.0	310	14	US-10-063-662-140	Sequence 140, App	211	100.0	310	14	US-10-063-587-140	Sequence 140, App
139	1617	100.0	310	14	US-10-063-510-140	Sequence 140, App	212	100.0	310	14	US-10-063-592-140	Sequence 140, App
140	1617	100.0	310	14	US-10-063-669-140	Sequence 140, App	213	100.0	310	14	US-10-063-597-140	Sequence 140, App
141	1617	100.0	310	14	US-10-063-670-140	Sequence 140, App	214	100.0	310	14	US-10-063-602-140	Sequence 140, App
142	1617	100.0	310	14	US-10-063-671-140	Sequence 140, App	215	100.0	310	14	US-10-063-606-140	Sequence 140, App
143	1617	100.0	310	14	US-10-063-674-140	Sequence 140, App	216	100.0	310	14	US-10-063-609-140	Sequence 140, App
144	1617	100.0	310	14	US-10-063-675-140	Sequence 140, App	217	100.0	310	14	US-10-063-611-140	Sequence 140, App
145	1617	100.0	310	14	US-10-063-676-140	Sequence 140, App	218	100.0	310	14	US-10-063-614-140	Sequence 140, App
146	1617	100.0	310	14	US-10-063-686-140	Sequence 140, App	219	100.0	310	14	US-10-063-639-140	Sequence 140, App
147	1617	100.0	310	14	US-10-063-689-140	Sequence 140, App	220	100.0	310	14	US-10-063-643-140	Sequence 140, App
148	1617	100.0	310	14	US-10-063-692-140	Sequence 140, App	221	100.0	310	14	US-10-063-646-140	Sequence 140, App
149	1617	100.0	310	14	US-10-063-693-140	Sequence 140, App	222	100.0	310	14	US-10-063-651-140	Sequence 140, App
150	1617	100.0	310	14	US-10-063-694-140	Sequence 140, App	223	100.0	310	14	US-10-063-653-140	Sequence 140, App
151	1617	100.0	310	14	US-10-063-698-140	Sequence 140, App	224	100.0	310	14	US-10-063-660-140	Sequence 140, App
152	1617	100.0	310	14	US-10-063-699-140	Sequence 140, App	225	100.0	310	14	US-10-063-665-140	Sequence 140, App
153	1617	100.0	310	14	US-10-063-702-140	Sequence 140, App	226	100.0	310	14	US-10-063-584-140	Sequence 140, App
154	1617	100.0	310	14	US-10-063-705-140	Sequence 140, App	227	100.0	310	14	US-10-063-536-140	Sequence 140, App
155	1617	100.0	310	14	US-10-063-707-140	Sequence 140, App	228	100.0	310	14	US-10-063-562-140	Sequence 140, App
156	1617	100.0	310	14	US-10-063-709-140	Sequence 140, App	229	100.0	310	14	US-10-063-638-140	Sequence 140, App
157	1617	100.0	310	14	US-10-063-713-140	Sequence 140, App	230	100.0	310	14	US-10-063-666-140	Sequence 140, App
158	1617	100.0	310	14	US-10-063-724-140	Sequence 140, App	231	100.0	310	14	US-10-063-672-140	Sequence 140, App
159	1617	100.0	310	14	US-10-063-727-140	Sequence 140, App	232	100.0	310	14	US-10-063-682-140	Sequence 140, App
160	1617	100.0	310	14	US-10-063-730-140	Sequence 140, App	233	100.0	310	14	US-10-063-721-140	Sequence 140, App
161	1617	100.0	310	14	US-10-063-734-140	Sequence 140, App	234	100.0	310	14	US-10-063-723-140	Sequence 140, App

2335	1617	100.0	310	14	US-10-063-514-140	Sequence 140, App	308	481	29.7	1089	12	US-10-196-757-266	Sequence 266, App
2336	1617	100.0	310	14	US-10-063-515-140	Sequence 140, App	309	481	29.7	1089	12	US-10-197-704-266	Sequence 266, App
2337	1617	100.0	310	14	US-10-063-523-140	Sequence 140, App	310	481	29.7	1089	12	US-10-197-710-266	Sequence 266, App
2338	1617	100.0	310	14	US-10-063-528-140	Sequence 140, App	311	481	29.7	1089	12	US-10-198-758-266	Sequence 266, App
2339	1617	100.0	310	14	US-10-063-688-140	Sequence 140, App	312	481	29.7	1089	12	US-10-198-766-266	Sequence 266, App
2340	1617	100.0	310	14	US-10-063-688-140	Sequence 140, App	313	481	29.7	1089	12	US-10-199-304-266	Sequence 266, App
2341	1617	100.0	310	14	US-10-063-688-140	Sequence 140, App	314	481	29.7	1089	12	US-10-199-309-266	Sequence 266, App
2342	1617	100.0	310	14	US-10-063-520-140	Sequence 140, App	315	481	29.7	1089	12	US-10-199-313-266	Sequence 266, App
2343	1617	100.0	310	14	US-10-063-647-140	Sequence 140, App	316	481	29.7	1089	12	US-10-199-456-266	Sequence 266, App
2344	1617	100.0	310	14	US-10-218-765-118	Sequence 118, App	317	481	29.7	1089	12	US-10-201-329-266	Sequence 266, App
2345	1617	100.0	310	14	US-10-219-066-118	Sequence 118, App	318	481	29.7	1089	12	US-10-202-413-266	Sequence 266, App
2346	1617	100.0	310	14	US-10-219-066-118	Sequence 118, App	319	481	29.7	1089	12	US-10-206-919-266	Sequence 266, App
2347	1617	100.0	310	14	US-10-219-066-118	Sequence 118, App	320	481	29.7	1089	12	US-10-206-924-266	Sequence 266, App
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2349	1617	100.0	310	14	US-10-219-068-118	Sequence 118, App	322	481	29.7	1089	12	US-10-206-928-266	Sequence 266, App
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2352	1617	100.0	310	14	US-10-219-475-118	Sequence 118, App	325	481	29.7	1089	12	US-10-207-922-266	Sequence 266, App
2353	1617	100.0	310	14	US-10-219-480-118	Sequence 118, App	326	481	29.7	1089	12	US-10-208-027-266	Sequence 266, App
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2355	1617	100.0	310	14	US-10-219-525-118	Sequence 118, App	328	481	29.7	1089	12	US-10-174-570-266	Sequence 266, App
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2358	1617	100.0	310	14	US-10-219-531-118	Sequence 118, App	331	481	29.7	1089	12	US-10-226-254A-102	Sequence 102, App
2359	1617	100.0	310	14	US-10-219-532-118	Sequence 118, App	332	481	29.7	1089	12	US-10-015-395A-102	Sequence 102, App
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2361	1617	100.0	310	14	US-10-232-228-118	Sequence 118, App	334	481	29.7	1089	14	US-10-174-590-266	Sequence 266, App
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2364	1617	100.0	310	14	US-10-063-578-140	Sequence 140, App	337	481	29.7	1089	14	US-10-175-737-266	Sequence 266, App
2365	1617	100.0	310	14	US-10-063-648-140	Sequence 140, App	338	481	29.7	1089	14	US-10-175-737-266	Sequence 266, App
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2368	1617	100.0	310	14	US-10-063-679-140	Sequence 140, App	341	481	29.7	1089	14	US-10-176-757-266	Sequence 266, App
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ALIGNMENTS

RESULT 1
US-09-931-836-45
; Sequence 45, Application US/09931836
; Publication No. US20030027249A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: F3030R1C1
; CURRENT APPLICATION NUMBER: US/09/931,836
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/085579

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; PRIOR APPLICATION NUMBER: 60/113430
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; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114140
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115552
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/125774
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125778
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125826
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/127035
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/127706
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/129122
; PRIOR FILING DATE: 1999-04-13
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; PRIOR APPLICATION NUMBER: 60/132383
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; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/138166
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; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/146970
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908, 827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 45
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-931-836-45

Query Match 100.0%; Score 1617; DB 10; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLGSGTFATCCVAIEVLGIAVFLRGFPAPVSSARAEHGAEPAPPSAGASSNWTTL 60
DB 1 MRLGSGTFATCCVAIEVLGIAVFLRGFPAPVSSARAEHGAEPAPPSAGASSNWTTL 60
QY 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKFWPYTYLVKSGASHSFVAEAKPPTVMPRIK 120
DB 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKFWPYTYLVKSGASHSFVAEAKPPTVMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWKLPPKHVEYDGT 180
DB 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWKLPPKHVEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDLILHLVGLDHIHSGNPSPLIGOKLSEMD 240
DB 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDLILHLVGLDHIHSGNPSPLIGOKLSEMD 240
QY 241 SVLMKIHTSLOSKEKETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
DB 241 SVLMKIHTSLOSKEKETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
DB 301 GDIRHPKHVQ 310

RESULT 2
US-10-081-056-292
; Sequence 292, Application US/10081056
; Publication No. US20040043927A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Marsters, Scott A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Ye, Weilan
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
 ; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
 ; FILE REFERENCE: P3235P1C1
 ; CURRENT APPLICATION NUMBER: US/10/081,056
 ; CURRENT FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: PCT/US01/21735
 ; PRIOR FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: US 60/219,556
 ; PRIOR FILING DATE: 2000-07-20
 ; PRIOR APPLICATION NUMBER: US 60/220,624
 ; PRIOR FILING DATE: 2000-07-25
 ; PRIOR APPLICATION NUMBER: US 60/220,664
 ; PRIOR FILING DATE: 2000-07-25
 ; PRIOR APPLICATION NUMBER: PCT/US00/20710
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: US 60/222,695
 ; PRIOR FILING DATE: 2000-08-02
 ; PRIOR APPLICATION NUMBER: US 09/643,657
 ; PRIOR FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: PCT/US00/23522
 ; PRIOR FILING DATE: 2000-08-23
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/230,978
 ; PRIOR FILING DATE: 2000-09-07
 ; PRIOR APPLICATION NUMBER: US 60/000,000
 ; PRIOR FILING DATE: 2000-09-15
 ; PRIOR APPLICATION NUMBER: US 09/664,610
 ; PRIOR FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: US 09/665,350
 ; PRIOR FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: US 60/242,922
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 09/709,238
 ; PRIOR FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: PCT/US00/30952
 ; PRIOR FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: PCT/US00/30873
 ; PRIOR FILING DATE: 2000-11-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678
 ; PRIOR FILING DATE: 2000-12-01
 ; PRIOR APPLICATION NUMBER: US 09/747,259
 ; PRIOR FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/34956
 ; PRIOR FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: US 09/767,609
 ; PRIOR FILING DATE: 2001-01-22
 ; PRIOR APPLICATION NUMBER: US 09/796,498
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: PCT/US01/06520
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: PCT/US01/06666
 ; PRIOR FILING DATE: 2001-03-01
 ; PRIOR APPLICATION NUMBER: US 09/802,706
 ; PRIOR FILING DATE: 2001-03-09
 ; PRIOR APPLICATION NUMBER: US 09/808,689
 ; PRIOR FILING DATE: 2001-03-14

; PRIOR APPLICATION NUMBER: US 09/816,744
 ; PRIOR FILING DATE: 2001-03-22
 ; PRIOR APPLICATION NUMBER: US 09/828,366
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: US 09/854,208
 ; PRIOR FILING DATE: 2001-05-10
 ; PRIOR APPLICATION NUMBER: US 09/854,280
 ; PRIOR FILING DATE: 2001-05-10
 ; PRIOR APPLICATION NUMBER: US 09/866,028
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: US 09/866,034
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: PCT/US01/17092
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: US 09/870,574
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/17443
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/17800
 ; PRIOR FILING DATE: 2001-06-01
 ; PRIOR APPLICATION NUMBER: PCT/US01/19692
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: PCT/US01/00000
 ; PRIOR FILING DATE: 2001-06-28
 ; NUMBER OF SEQ ID NOS: 383
 ; SEQ ID NO 292
 ; LENGTH: 310
 ; TYPE: PRT
 ; ORGANISM: Homosapiens
 ; US-10-081-056-292
 Query Match 100.0%; Score 1617; DB 12; Length 310;
 Best Local Similarity 100.0%; Pred. No. 1.4e-155; Indels 0; Gaps 0;
 Matches 310; Conservative 0; Mismatches 0
 Qy 1 MRLSGTTFATCCVAIEVLGIAVFLRGFFFPAPVRSSARAHEGAEPPAPPSAGASSNWTL 60
 Db 1 MRLSGTTFATCCVAIEVLGIAVFLRGFFFPAPVRSSARAHEGAEPPAPPSAGASSNWTL 60
 Qy 61 PPPLFSKVIILDALRDDVFGSKGVKMPYTYLVEKGASHSFVAEAKPTVTMPRIK 120
 Db 61 PPPLFSKVIILDALRDDVFGSKGVKMPYTYLVEKGASHSFVAEAKPTVTMPRIK 120
 Qy 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDVTWVLFPPKHFEYDGT 180
 Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDVTWVLFPPKHFEYDGT 180
 Qy 181 TSFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHIGSPNSFLICQKLSMD 240
 Db 181 TSFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHIGSPNSFLICQKLSMD 240
 Qy 241 SVLMKHTSLQSKERTPLPDLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
 Db 241 SVLMKHTSLQSKERTPLPDLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
 Qy 301 GDIRHPKHVQ 310
 Db 301 GDIRHPKHVQ 310

RESULT 3
 US-10-219-535-118
 ; Sequence 118, Application US/10219535
 ; Publication No. US20040044179A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PIC60
CURRENT APPLICATION NUMBER: US/10/219,535
PRIOR FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 118
TYPE: PRT
LENGTH: 310
ORGANISM: Homo Sapien
US-10-219-535-118

Query Match 100.0%; Score 1617; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLSGTFTATCCVAIEVLGIAVFLRGFFPAPVRSSARAHEGAEPAPPEPSAGASSNWTTL 60
DB 1 MRLSGTFTATCCVAIEVLGIAVFLRGFFPAPVRSSARAHEGAEPAPPEPSAGASSNWTTL 60
QY 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTVLVEKGASHSFVAEAKPPTVTMPRIK 120
DB 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTVLVEKGASHSFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVSVIROAKAAGKRIIFYGDETWWKLPFKHFVEYDGT 180
DB 121 ALMTGSLPGFVDVIRNLNSPALLEDVSVIROAKAAGKRIIFYGDETWWKLPFKHFVEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHIGSPNSPLIGQKLSMD 240
DB 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHIGSPNSPLIGQKLSMD 240
QY 241 SVLMKIHTSLOSKERETPLPNLILVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
DB 241 SVLMKIHTSLOSKERETPLPNLILVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
DB 301 GDIRHPKHVQ 310

RESULT 5
US-10-063-745-140
Sequence 140, Application US/10063745

APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PIC60
CURRENT APPLICATION NUMBER: US/10/219,535
PRIOR FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 118
TYPE: PRT
LENGTH: 310
ORGANISM: Homo Sapien
US-10-219-535-118

Query Match 100.0%; Score 1617; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLSGTFTATCCVAIEVLGIAVFLRGFFPAPVRSSARAHEGAEPAPPEPSAGASSNWTTL 60
DB 1 MRLSGTFTATCCVAIEVLGIAVFLRGFFPAPVRSSARAHEGAEPAPPEPSAGASSNWTTL 60
QY 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTVLVEKGASHSFVAEAKPPTVTMPRIK 120
DB 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTVLVEKGASHSFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVSVIROAKAAGKRIIFYGDETWWKLPFKHFVEYDGT 180
DB 121 ALMTGSLPGFVDVIRNLNSPALLEDVSVIROAKAAGKRIIFYGDETWWKLPFKHFVEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHIGSPNSPLIGQKLSMD 240
DB 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHIGSPNSPLIGQKLSMD 240
QY 241 SVLMKIHTSLOSKERETPLPNLILVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
DB 241 SVLMKIHTSLOSKERETPLPNLILVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
DB 301 GDIRHPKHVQ 310

RESULT 4
US-10-232-230-118
Sequence 118, Application US/10232230
Publication No. US20040044180A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary

```
; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230RIC1
; CURRENT APPLICATION NUMBER: US/10/063,745
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 140
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-745-140

Query Match      100.0%; Score 1617; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLGSGTATCCVAIEVLGIAVFLRGFFPAPVRSARAEGHGAEPAPPSAGASSNWTTL 60
Db 1 MRLGSGTATCCVAIEVLGIAVFLRGFFPAPVRSARAEGHGAEPAPPSAGASSNWTTL 60
QY 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTVLVEKGASHSFVAEAKPPTVTMPRIK 120
Db 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTVLVEKGASHSFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLESVIRQAAAGKRIVFYGDETWVKLFPKHFEYDGT 180
Db 121 ALMTGSLPGFVDVIRNLNSPALLESVIRQAAAGKRIVFYGDETWVKLFPKHFEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHIGSPNSPLIGQKLSMD 240
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHIGSPNSPLIGQKLSMD 240
QY 241 SVLMKIHTSLOSKERETPLPNLLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
Db 241 SVLMKIHTSLOSKERETPLPNLLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
Db 301 GDIRHPKHVQ 310

RESULT 7
US-10-063-513-140
; Sequence 140, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230RIC1
; CURRENT APPLICATION NUMBER: US/10/063,513
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 140
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-513-140

Query Match      100.0%; Score 1617; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLGSGTATCCVAIEVLGIAVFLRGFFPAPVRSARAEGHGAEPAPPSAGASSNWTTL 60
Db 1 MRLGSGTATCCVAIEVLGIAVFLRGFFPAPVRSARAEGHGAEPAPPSAGASSNWTTL 60
QY 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTVLVEKGASHSFVAEAKPPTVTMPRIK 120
Db 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTVLVEKGASHSFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLESVIRQAAAGKRIVFYGDETWVKLFPKHFEYDGT 180
Db 121 ALMTGSLPGFVDVIRNLNSPALLESVIRQAAAGKRIVFYGDETWVKLFPKHFEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHIGSPNSPLIGQKLSMD 240
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIHIGSPNSPLIGQKLSMD 240
QY 241 SVLMKIHTSLOSKERETPLPNLLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
Db 241 SVLMKIHTSLOSKERETPLPNLLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
Db 301 GDIRHPKHVQ 310

RESULT 6
US-10-063-512-140
; Sequence 140, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230RIC1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
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Db 61 PPPLFSKVIVLIDALRDDVFVSGKGVKMPYTYLVEKGASHSFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVSVIROKAAGKRIIVFYGDETWVKLPFKHFEVDGT 180
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVSVIROKAAGKRIIVFYGDETWVKLPFKHFEVDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHIGSGNSPLIGQKLEMD 240
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHIGSGNSPLIGQKLEMD 240
QY 241 SVLMKIHTSLOSKERETPLPNNLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
Db 241 SVLMKIHTSLOSKERETPLPNNLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
Db 301 GDIRHPKHVQ 310

RESULT 8

US-10-063-515-140
; Sequence 140, Application US/10063515

; Publication No. US20030018173A1

; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3230R1C1

; CURRENT APPLICATION NUMBER: US/10/063,515

; CURRENT FILING DATE: 2002-05-01

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 170

; SEQ ID NO 140

; LENGTH: 310

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-063-515-140

Query Match 100.0%; Score 1617; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPEPSAGASSNWTL 60
Db 1 MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPEPSAGASSNWTL 60
QY 61 PPPLFSKVIVLIDALRDDVFVSGKGVKMPYTYLVEKGASHSFVAEAKPPTVTMPRIK 120
Db 61 PPPLFSKVIVLIDALRDDVFVSGKGVKMPYTYLVEKGASHSFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVSVIROKAAGKRIIVFYGDETWVKLPFKHFEVDGT 180
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVSVIROKAAGKRIIVFYGDETWVKLPFKHFEVDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHIGSGNSPLIGQKLEMD 240
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHIGSGNSPLIGQKLEMD 240
QY 241 SVLMKIHTSLOSKERETPLPNNLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
Db 241 SVLMKIHTSLOSKERETPLPNNLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
Db 301 GDIRHPKHVQ 310

RESULT 9

US-10-063-549-140

; Sequence 140, Application US/10063549

; Publication No. US20030027986A1

; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3230R1C1

; CURRENT APPLICATION NUMBER: US/10/063,549

; CURRENT FILING DATE: 2002-05-02

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 170

; SEQ ID NO 140

; LENGTH: 310

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-063-549-140

Query Match 100.0%; Score 1617; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPEPSAGASSNWTL 60
Db 1 MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGHGAEPAPPEPSAGASSNWTL 60
QY 61 PPPLFSKVIVLIDALRDDVFVSGKGVKMPYTYLVEKGASHSFVAEAKPPTVTMPRIK 120
Db 61 PPPLFSKVIVLIDALRDDVFVSGKGVKMPYTYLVEKGASHSFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVSVIROKAAGKRIIVFYGDETWVKLPFKHFEVDGT 180
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVSVIROKAAGKRIIVFYGDETWVKLPFKHFEVDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHIGSGNSPLIGQKLEMD 240
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHIGSGNSPLIGQKLEMD 240
QY 241 SVLMKIHTSLOSKERETPLPNNLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
Db 241 SVLMKIHTSLOSKERETPLPNNLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
Db 301 GDIRHPKHVQ 310

RESULT 10

US-10-063-569-140

; Sequence 140, Application US/10063569

; Publication No. US20030018168A1

; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

```

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,569
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 140
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-551-140

Query Match      100.0%; Score 1617; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLGSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPAPPSAGASSNWTL 60
Db 1 MRLGSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPAPPSAGASSNWTL 60
QY 61 PPPLFSKVIVLIDALRDDDFVFGSGKGVKMPYTTVLVEKGASHSFVAEAKPPTVTMPRIK 120
Db 61 PPPLFSKVIVLIDALRDDDFVFGSGKGVKMPYTTVLVEKGASHSFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGRIIVFYGDETWWKLFPPKHFEYDGT 180
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGRIIVFYGDETWWKLFPPKHFEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHLGHISGPNPLIGQKLSMD 240
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHLGHISGPNPLIGQKLSMD 240
QY 241 SVLMKHTISLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
Db 241 SVLMKHTISLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
Db 301 GDIRHPKHVQ 310

RESULT 11
US-10-063-551-140
; Sequence 140, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 140
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-551-140

Query Match      100.0%; Score 1617; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLGSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPAPPSAGASSNWTL 60
Db 1 MRLGSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPAPPSAGASSNWTL 60
QY 61 PPPLFSKVIVLIDALRDDDFVFGSGKGVKMPYTTVLVEKGASHSFVAEAKPPTVTMPRIK 120
Db 61 PPPLFSKVIVLIDALRDDDFVFGSGKGVKMPYTTVLVEKGASHSFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGRIIVFYGDETWWKLFPPKHFEYDGT 180
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGRIIVFYGDETWWKLFPPKHFEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHLGHISGPNPLIGQKLSMD 240
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHLGHISGPNPLIGQKLSMD 240
QY 241 SVLMKHTISLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
Db 241 SVLMKHTISLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
Db 301 GDIRHPKHVQ 310

US-10-063-551-140
; Sequence 140, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 140
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-551-140

Query Match      100.0%; Score 1617; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLGSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPAPPSAGASSNWTL 60

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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,569
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 140
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-551-140

Query Match      100.0%; Score 1617; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLGSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPAPPSAGASSNWTL 60
Db 1 MRLGSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPAPPSAGASSNWTL 60
QY 61 PPPLFSKVIVLIDALRDDDFVFGSGKGVKMPYTTVLVEKGASHSFVAEAKPPTVTMPRIK 120
Db 61 PPPLFSKVIVLIDALRDDDFVFGSGKGVKMPYTTVLVEKGASHSFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGRIIVFYGDETWWKLFPPKHFEYDGT 180
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGRIIVFYGDETWWKLFPPKHFEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHLGHISGPNPLIGQKLSMD 240
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHLGHISGPNPLIGQKLSMD 240
QY 241 SVLMKHTISLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
Db 241 SVLMKHTISLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
Db 301 GDIRHPKHVQ 310

RESULT 12
US-10-063-555-140
; Sequence 140, Application US/10063555
; Publication No. US20030065143A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,555
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 140
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-555-140

Query Match      100.0%; Score 1617; DB 12; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.4e-155;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLGSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPAPPSAGASSNWTL 60
Db 1 MRLGSGTFCATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPAPPSAGASSNWTL 60
QY 61 PPPLFSKVIVLIDALRDDDFVFGSGKGVKMPYTTVLVEKGASHSFVAEAKPPTVTMPRIK 120
Db 61 PPPLFSKVIVLIDALRDDDFVFGSGKGVKMPYTTVLVEKGASHSFVAEAKPPTVTMPRIK 120
QY 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGRIIVFYGDETWWKLFPPKHFEYDGT 180
Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGRIIVFYGDETWWKLFPPKHFEYDGT 180
QY 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHLGHISGPNPLIGQKLSMD 240
Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHLGHISGPNPLIGQKLSMD 240
QY 241 SVLMKHTISLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
Db 241 SVLMKHTISLOSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKP 300
QY 301 GDIRHPKHVQ 310
Db 301 GDIRHPKHVQ 310

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Db 241 SVLMKIHTSLOSKERETPLNLLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
 Qy 301 GDIRHPKHVQ 310
 Db 301 GDIRHPKHVQ 310

RESULT 13
 US-10-063-563-140
 ; Sequence 140, Application US/10063563
 ; Publication No. US20030060502A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,563
 ; CURRENT FILING DATE: 2002-05-02
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 140
 ; LENGTH: 310
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-063-563-140

Query Match 100.0%; Score 1617; DB 12; Length 310;
 Best Local Similarity 100.0%; Pred. No. 1.4e-155;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRLSGTATCCVAIEVLGIAVFLRGFFPAPVRSSARAHEGAEPPAPPSAGASSNWTTL 60
 Db 1 MRLSGTATCCVAIEVLGIAVFLRGFFPAPVRSSARAHEGAEPPAPPSAGASSNWTTL 60

Qy 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTYLVEKGASHSFVAEAKPPTVMPRIK 120
 Db 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTYLVEKGASHSFVAEAKPPTVMPRIK 120

Qy 121 ALMTGSLPGFVDVIRNLNSPALLEDVSIRQAKAAGKRIVFYGDETWVKLPKHFEVDGT 180
 Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVSIRQAKAAGKRIVFYGDETWVKLPKHFEVDGT 180

Qy 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHISGNSPLIGQKLEMD 240
 Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHISGNSPLIGQKLEMD 240

Qy 241 SVLMKIHTSLOSKERETPLNLLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
 Db 241 SVLMKIHTSLOSKERETPLNLLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300

Qy 301 GDIRHPKHVQ 310
 Db 301 GDIRHPKHVQ 310

RESULT 14
 US-10-063-594-140
 ; Sequence 140, Application US/10063594
 ; Publication No. US20030065161A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,594
 ; CURRENT FILING DATE: 2002-05-30
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 140
 ; LENGTH: 310
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-063-594-140

Query Match 100.0%; Score 1617; DB 12; Length 310;
 Best Local Similarity 100.0%; Pred. No. 1.4e-155;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRLSGTATCCVAIEVLGIAVFLRGFFPAPVRSSARAHEGAEPPAPPSAGASSNWTTL 60
 Db 1 MRLSGTATCCVAIEVLGIAVFLRGFFPAPVRSSARAHEGAEPPAPPSAGASSNWTTL 60

Qy 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTYLVEKGASHSFVAEAKPPTVMPRIK 120
 Db 61 PPPLFSKVIVLIDALRDDDFVFGSKGVKMPYTTYLVEKGASHSFVAEAKPPTVMPRIK 120

Qy 121 ALMTGSLPGFVDVIRNLNSPALLEDVSIRQAKAAGKRIVFYGDETWVKLPKHFEVDGT 180
 Db 121 ALMTGSLPGFVDVIRNLNSPALLEDVSIRQAKAAGKRIVFYGDETWVKLPKHFEVDGT 180

Qy 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHISGNSPLIGQKLEMD 240
 Db 181 TSFFVSDYTEVDNNVTRHLDKVLKRGDWDILILHVLGLDHIHISGNSPLIGQKLEMD 240

Qy 241 SVLMKIHTSLOSKERETPLNLLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300
 Db 241 SVLMKIHTSLOSKERETPLNLLVLCGDHGMSETSGHSGASSTEEVNTPLILISSAFERKP 300

Qy 301 GDIRHPKHVQ 310
 Db 301 GDIRHPKHVQ 310

RESULT 15
 US-10-063-553-140
 ; Sequence 140, Application US/10063553
 ; Publication No. US20030045684A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,553
 ; CURRENT FILING DATE: 2002-05-02
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 140
 ; LENGTH: 310
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-063-553-140

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 2, 2004, 16:27:33 ; Search time 19 seconds

(without alignments)
842.318 Million cell updates/sec

Title: US-10-036-150-45

Perfect score: 1617

Sequence: 1 MRLSGTFCATCCVAIEVLGI.....LISSAFERKPGDIRPKHVQ 310

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Issued Patents 1A.*

1: /cgn2_6/prodata/2/iaa/5A COMB.pep.*

2: /cgn2_6/prodata/2/iaa/5B COMB.pep.*

3: /cgn2_6/prodata/2/iaa/6A COMB.pep.*

4: /cgn2_6/prodata/2/iaa/6B COMB.pep.*

5: /cgn2_6/prodata/2/iaa/PCUTS COMB.pep.*

6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	220.5	13.6	185	4	US-09-621-976-4112 Sequence 4112, Ap
2	170	10.5	287	4	US-09-252-991A-21605 Sequence 21605, A
3	148	9.2	275	4	US-09-540-236-2033 Sequence 2033, Ap
4	139	8.6	355	2	US-09-014-969-19 Sequence 19, Appl
5	127	7.9	438	4	US-09-187-331-2 Sequence 2, Appli
6	127	7.9	438	4	US-09-470-946-2 Sequence 6, Appli
7	101	6.2	873	3	US-09-187-331-6 Sequence 6, Appli
8	101	6.2	873	4	US-09-470-946-6 Sequence 6, Appli
9	101	6.2	873	4	US-09-438-906-2 Sequence 4, Appli
10	101	6.2	873	4	US-09-438-906-4 Sequence 4, Appli
11	101	6.2	925	2	US-08-392-946-1 Sequence 1, Appli
12	101	6.2	925	2	US-08-504-169-1 Sequence 1, Appli
13	101	6.2	925	5	PCT-US94-14893-1 Sequence 4717, Ap
14	99	6.1	230	4	US-09-107-532A-4717 Sequence 6, Appli
15	96.5	6.0	2109	3	US-08-646-695-6 Sequence 6, Appli
16	96.5	6.0	2109	5	PCT-US96-06053-6 Sequence 18, Appl
17	95	5.9	311	4	US-09-277-716-18 Sequence 18, Appl
18	95	5.9	311	4	US-09-609-161B-18 Sequence 18, Appl
19	94.5	5.8	686	4	US-09-252-991A-26437 Sequence 7, Appli
20	92	5.7	331	2	US-08-386-217-7 Sequence 5, Appli
21	92	5.7	333	4	US-09-562-737-5 Sequence 5, Appli
22	92	5.7	620	3	US-09-000-145-5 Sequence 5, Appli
23	89.5	5.5	796	3	US-08-961-083-56 Sequence 56, Appl
24	89.5	5.5	796	4	US-09-536-784-56 Sequence 56, Appl
25	89	5.5	1245	4	US-09-543-681A-5592 Sequence 5592, Ap
26	88.5	5.5	470	4	US-09-266-965-118 Sequence 118, App
27	88.5	5.5	819	4	US-09-468-656A-8 Sequence 8, Appli

28	87.5	5.4	911	1	US-08-596-985-2 Sequence 2, Appli
29	87	5.4	311	3	US-09-330-317B-2 Sequence 2, Appli
30	87	5.4	311	4	US-09-808-589A-2 Sequence 2, Appli
31	87	5.4	339	3	US-09-330-317B-4 Sequence 4, Appli
32	87	5.4	339	3	US-09-330-317B-10 Sequence 10, Appl
33	87	5.4	339	3	US-09-330-317B-12 Sequence 12, Appl
34	87	5.4	339	3	US-09-330-317B-14 Sequence 14, Appl
35	87	5.4	339	3	US-09-330-317B-16 Sequence 16, Appl
36	87	5.4	339	4	US-09-808-589A-4 Sequence 4, Appli
37	87	5.4	339	4	US-09-808-589A-10 Sequence 10, Appl
38	87	5.4	339	4	US-09-808-589A-12 Sequence 12, Appl
39	87	5.4	339	4	US-09-808-589A-14 Sequence 14, Appl
40	87	5.4	339	4	US-09-808-589A-16 Sequence 16, Appl
41	86	5.3	657	4	US-09-252-991A-27358 Sequence 27358, A
42	86	5.3	861	1	US-08-346-455B-67 Sequence 67, Appl
43	86	5.3	861	3	US-08-977-321-67 Sequence 67, Appl
44	86	5.3	861	4	US-09-483-811B-67 Sequence 2, Appli
45	86	5.3	861	4	US-09-784-316-2 Sequence 2, Appli
46	86	5.3	861	5	PCT-US95-08613-67 Sequence 67, Appl
47	85	5.3	1098	1	US-08-290-301-82 Sequence 82, Appl
48	85	5.3	1098	4	US-09-013-598-82 Sequence 82, Appl
49	84.5	5.2	368	3	US-08-972-902-2 Sequence 2, Appli
50	84.5	5.2	368	4	US-09-520-207-2 Sequence 2, Appli
51	84.5	5.2	368	4	US-10-136-253-2 Sequence 2, Appli
52	83.5	5.2	903	1	US-08-750-532-1 Sequence 1, Appli
53	83.5	5.2	1398	1	US-08-750-532-9 Sequence 9, Appli
54	83.5	5.2	1398	3	US-08-894-818B-8 Sequence 8, Appli
55	83.5	5.2	1398	4	US-09-445-472-6 Sequence 6, Appli
56	82.5	5.1	266	4	US-09-489-039A-8199 Sequence 8199, Ap
57	82.5	5.1	575	4	US-09-071-035-296 Sequence 296, App
58	82.5	5.1	601	4	US-09-071-035-294 Sequence 294, App
59	82	5.1	344	4	US-09-252-991A-31357 Sequence 31357, A
60	82	5.1	1091	3	US-09-306-595C-7 Sequence 7, Appli
61	82	5.1	1091	4	US-09-925-388-7 Sequence 7, Appli
62	81.5	5.0	502	4	US-09-252-991A-30007 Sequence 30007, A
63	81.5	5.0	521	4	US-09-328-352-5423 Sequence 5423, Ap
64	81	5.0	235	4	US-09-107-532A-6882 Sequence 6882, Ap
65	81	5.0	313	3	US-09-347-803-6 Sequence 6, Appli
66	81	5.0	360	4	US-09-252-991A-19088 Sequence 19088, A
67	81	5.0	1394	4	US-09-845-917A-57 Sequence 57, Appl
68	81	5.0	1449	4	US-09-845-917A-58 Sequence 58, Appl
69	81	5.0	1528	4	US-09-845-917A-3 Sequence 3, Appli
70	81	5.0	1583	4	US-09-845-917A-4 Sequence 4, Appli
71	81	5.0	1890	4	US-09-004-838-88 Sequence 88, Appl
72	80	4.9	604	4	US-09-391-104-30 Sequence 30, Appl
73	80	4.9	1817	4	US-09-004-838-125 Sequence 125, App
74	79.5	4.9	911	4	US-08-461-562B-2 Sequence 2, Appli
75	79.5	4.9	986	4	US-09-403-618A-5 Sequence 5, Appli
76	79	4.9	427	4	US-08-065-844A-2 Sequence 2, Appli
77	79	4.9	444	4	US-09-328-352-7043 Sequence 7043, Ap
78	78.5	4.9	287	4	US-09-252-991A-19272 Sequence 19272, A
79	78.5	4.9	338	4	US-09-489-039A-10172 Sequence 10172, A
80	78.5	4.9	364	4	US-09-437-485D-46 Sequence 46, Appl
81	78.5	4.9	388	4	US-09-331-586A-4 Sequence 4, Appli
82	78.5	4.9	388	4	US-09-331-586A-29 Sequence 29, Appl
83	78.5	4.9	409	4	US-09-540-236-3384 Sequence 3384, Ap
84	78.5	4.9	775	2	US-08-714-677-4 Sequence 4, Appli
85	78.5	4.9	775	2	US-08-393-540-4 Sequence 4, Appli
86	78.5	4.9	775	4	US-08-714-677-4 Sequence 4, Appli
87	78	4.8	437	1	US-08-136-119-4 Sequence 13, Appl
88	78	4.8	437	2	US-08-723-415B-13 Sequence 13, Appl
89	78	4.8	437	3	US-08-481-814A-6 Sequence 6, Appli
90	78	4.8	437	3	US-08-801-092-1 Sequence 1, Appli
91	78	4.8	437	3	US-09-189-627A-13 Sequence 13, Appl
92	78	4.8	437	4	US-09-242-737-2 Sequence 2, Appli
93	78	4.8	437	4	US-09-315-113-1 Sequence 1, Appli
94	78	4.8	437	4	US-09-710-861-13 Sequence 13, Appl
95	78	4.8	476	2	US-08-139-937-14 Sequence 14, Appl
96	78	4.8	476	5	PCT-US93-11310-14 Sequence 14, Appl
97	78	4.8	607	3	US-09-000-041A-2 Sequence 2, Appli
98	77.5	4.8	392	4	US-09-134-000C-6542 Sequence 6542, Ap
99	77.5	4.8	521	4	US-09-134-001C-4290 Sequence 4290, Ap
100	77.5	4.8	582	3	US-08-906-865-3 Sequence 3, Appli

101	77.5	4.8	582	4	US-09-129-668-3	Sequence 3, Appli	174	73.5	4.5	511	4	US-09-328-352-6176	Sequence 6176, Ap
102	77.5	4.8	865	4	US-09-281-766-19	Sequence 19, Appli	175	73.5	4.5	517	4	US-09-134-001C-5444	Sequence 5444, Ap
103	77	4.8	213	4	US-09-540-236-2742	Sequence 2742, Ap	176	73.5	4.5	526	4	US-09-232-991A-2748	Sequence 2748, A
104	77	4.8	412	2	US-08-414-938A-4	Sequence 4, Appli	177	73.5	4.5	565	4	US-09-489-039A-10676	Sequence 10676, A
105	77	4.8	541	4	US-09-614-913-66	Sequence 66, Appli	178	73.5	4.5	566	4	US-09-489-039A-4908	Sequence 4908, Ap
106	76.5	4.7	170	3	US-09-130-663-2	Sequence 2, Appli	179	73	4.5	317	4	US-09-352-991A-29954	Sequence 29954, A
107	76.5	4.7	170	3	US-09-432-335-2	Sequence 2, Appli	180	73	4.5	344	2	US-08-690-493-1	Sequence 1, Appli
108	76.5	4.7	170	3	US-09-614-022-2	Sequence 2, Appli	181	73	4.5	650	4	US-09-134-001C-4444	Sequence 4444, Ap
109	76.5	4.7	237	4	US-09-134-001C-5631	Sequence 5631, Ap	182	73	4.5	686	4	US-09-107-532A-5205	Sequence 5205, Ap
110	76.5	4.7	711	4	US-09-485-737B-90	Sequence 90, Appli	183	73	4.5	863	4	US-09-562-737-46	Sequence 46, Appli
111	76.5	4.7	763	4	US-09-328-352-4406	Sequence 4406, Ap	184	73	4.5	1024	4	US-09-430-633-1	Sequence 1, Appli
112	76.5	4.7	1565	4	US-08-551-567B-59	Sequence 59, Appli	185	72.5	4.5	223	1	US-08-936-854-1	Sequence 1, Appli
113	76	4.7	306	4	US-09-543-681A-7494	Sequence 7494, Ap	186	72.5	4.5	223	3	US-08-928-361B-7	Sequence 7, Appli
114	76	4.7	437	1	US-07-882-711-2	Sequence 2, Appli	187	72.5	4.5	303	4	US-09-588-958A-7	Sequence 7, Appli
115	76	4.7	437	2	US-08-462-174-2	Sequence 2, Appli	188	72.5	4.5	326	2	US-08-986-217-3	Sequence 3, Appli
116	76	4.7	581	4	US-09-352-991A-17734	Sequence 17734, A	189	72.5	4.5	369	2	US-08-596-231-4	Sequence 4, Appli
117	76	4.7	620	3	US-09-000-145-3	Sequence 3, Appli	190	72.5	4.5	369	3	US-09-100-804-4	Sequence 4, Appli
118	76	4.7	718	4	US-09-107-532A-5234	Sequence 5234, Ap	191	72.5	4.5	369	4	US-09-489-039A-10540	Sequence 10540, A
119	76	4.7	935	2	US-08-152-721B-2	Sequence 2, Appli	192	72.5	4.5	369	5	PCT-US94-09943-4	Sequence 4, Appli
120	76	4.7	1289	2	US-08-853-658A-51	Sequence 51, Appli	193	72.5	4.5	393	4	US-09-543-681A-5865	Sequence 5865, Ap
121	76	4.7	2366	1	US-08-480-604A-10	Sequence 10, Appli	194	72.5	4.5	393	4	US-09-543-681A-4386	Sequence 4386, Ap
122	76	4.7	2366	3	US-08-405-496A-10	Sequence 10, Appli	195	72.5	4.5	416	4	US-09-489-039A-13738	Sequence 13738, A
123	76	4.7	2366	3	US-08-915-136-10	Sequence 10, Appli	196	72.5	4.5	429	4	US-09-489-039A-11164	Sequence 11164, A
124	76	4.7	2366	4	US-08-957-310-10	Sequence 10, Appli	197	72.5	4.5	479	4	US-09-489-039A-9208	Sequence 9208, Ap
125	76	4.7	2366	4	US-10-011-366-10	Sequence 10, Appli	198	72.5	4.5	499	4	US-09-107-532A-5564	Sequence 5564, Ap
126	76	4.7	2366	4	US-09-084-517-10	Sequence 10, Appli	199	72.5	4.5	550	4	US-07-683-957B-2	Sequence 2, Appli
127	75.5	4.7	333	4	US-09-562-737-2	Sequence 2, Appli	200	72.5	4.5	575	1	US-09-543-681A-5296	Sequence 5296, Ap
128	75.5	4.7	472	4	US-09-625-188-6	Sequence 6, Appli	201	72.5	4.5	579	4	US-09-136-574A-47	Sequence 47, Appli
129	75.5	4.7	512	2	US-08-557-122A-33	Sequence 33, Appli	202	72.5	4.5	616	3	US-09-107-532A-6065	Sequence 6065, Ap
130	75.5	4.7	512	2	US-09-262-666-33	Sequence 33, Appli	203	72.5	4.5	791	2	US-08-775-009-35	Sequence 35, Appli
131	75	4.6	441	4	US-09-328-352-5114	Sequence 5114, Ap	204	72.5	4.5	885	2	US-08-500-857A-8	Sequence 8, Appli
132	75	4.6	485	4	US-09-489-039A-10554	Sequence 10554, A	205	72.5	4.5	1426	3	US-09-136-574A-43	Sequence 43, Appli
133	75	4.6	486	4	US-09-489-039A-7787	Sequence 7787, Ap	206	72.5	4.5	1837	3	US-08-928-361B-5	Sequence 5, Appli
134	75	4.6	547	1	US-08-785-048-3	Sequence 3, Appli	207	72.5	4.5	1837	4	US-09-588-995A-5	Sequence 5, Appli
135	75	4.6	547	2	US-08-966-799-3	Sequence 3, Appli	208	72.5	4.5	2319	1	US-08-212-133A-8	Sequence 8, Appli
136	75	4.6	553	1	US-08-785-048-2	Sequence 2, Appli	209	72.5	4.5	2319	1	US-08-474-503-6	Sequence 6, Appli
137	75	4.6	553	2	US-08-996-799-2	Sequence 2, Appli	210	72.5	4.5	2319	2	US-08-670-707A-6	Sequence 6, Appli
138	75	4.6	582	4	US-09-252-991A-29341	Sequence 29341, A	211	72.5	4.5	2319	3	US-09-315-179-6	Sequence 6, Appli
139	75	4.6	582	2	US-08-449-645A-18	Sequence 18, Appli	212	72.5	4.5	2319	4	US-09-523-656-28	Sequence 28, Appli
140	75	4.6	976	2	US-08-702-367A-18	Sequence 18, Appli	213	72.5	4.5	2319	5	PCT-US94-13200-6	Sequence 6, Appli
141	75	4.6	976	5	US-08-966-799-3	Sequence 3, Appli	214	72.5	4.5	3072	3	US-09-413-814-93	Sequence 93, Appli
142	74.5	4.6	250	4	US-09-252-991A-32751	Sequence 32751, A	215	72.5	4.5	3073	3	US-09-413-814-80	Sequence 80, Appli
143	74.5	4.6	474	4	US-08-403-866-1	Sequence 1, Appli	216	72.5	4.5	182	3	US-09-338-307-133	Sequence 133, App
144	74.5	4.6	513	1	US-09-773-426A-7	Sequence 7, Appli	217	72	4.5	182	4	US-09-218-207-11	Sequence 11, Appli
145	74.5	4.6	599	4	US-08-484-993B-10	Sequence 10, Appli	218	72	4.5	324	2	US-08-671-320-11	Sequence 11, Appli
146	74.5	4.6	715	2	US-08-484-158B-10	Sequence 10, Appli	219	72	4.5	324	2	US-08-868-577-11	Sequence 11, Appli
147	74.5	4.6	715	2	US-08-484-596A-10	Sequence 10, Appli	220	72	4.5	324	2	US-09-207-914-11	Sequence 9, Appli
148	74.5	4.6	715	2	US-08-480-150A-10	Sequence 10, Appli	221	72	4.5	451	3	US-09-371-913A-9	Sequence 9, Appli
149	74.5	4.6	715	2	US-08-458-731-10	Sequence 10, Appli	222	72	4.5	451	4	US-09-967-805-9	Sequence 7, Appli
150	74.5	4.6	715	3	US-08-149-223A-10	Sequence 10, Appli	223	72	4.5	516	2	US-09-252-991A-24185	Sequence 24185, A
151	74.5	4.6	879	4	US-09-107-532A-4679	Sequence 4679, Ap	224	72	4.5	588	4	US-09-489-039A-8996	Sequence 8996, Ap
152	74.5	4.6	1041	1	US-08-220-151-4	Sequence 4, Appli	225	72	4.5	638	4	US-09-059-584-49	Sequence 49, Appli
153	74.5	4.6	1041	1	US-08-413-118-4	Sequence 4, Appli	226	72	4.5	713	4	US-09-233-857-13	Sequence 13, Appli
154	74.5	4.6	1041	3	US-08-473-446-4	Sequence 4, Appli	227	72	4.5	1088	4	US-09-442-100-2	Sequence 2, Appli
155	74.5	4.6	1708	4	US-09-462-606-2	Sequence 2, Appli	228	72	4.5	1088	4	US-09-939-106-2	Sequence 2, Appli
156	74.5	4.6	355	4	US-09-574-377-12	Sequence 12, Appli	229	72	4.5	1099	4	US-08-442-102-2	Sequence 2, Appli
157	74	4.6	460	4	US-09-266-965-126	Sequence 126, App	230	72	4.5	1099	4	US-09-075-272-4	Sequence 4, Appli
158	74	4.6	607	3	US-09-211-704A-10	Sequence 10, Appli	231	72	4.5	1203	3	US-09-413-814-28	Sequence 28, Appli
159	74	4.6	612	1	US-08-344-695-2	Sequence 2, Appli	232	72	4.5	1341	4	US-09-540-336-3044	Sequence 3044, Ap
160	74	4.6	709	4	US-09-668-673B-3	Sequence 3, Appli	233	72	4.5	2618	3	US-09-562-737-6	Sequence 6, Appli
161	74	4.6	715	4	US-09-107-532A-4219	Sequence 4219, Ap	234	72	4.5	2618	4	US-09-198-452A-38	Sequence 38, Appli
162	74	4.6	831	4	US-08-623-326-43	Sequence 43, Appli	235	72	4.5	333	4	US-09-501-115-12	Sequence 12, Appli
163	74	4.6	946	4	US-09-252-991A-18989	Sequence 18989, A	236	71.5	4.4	333	4	US-09-489-039A-10807	Sequence 10807, A
164	74	4.6	946	4	US-08-500-857A-8	Sequence 2, Appli	237	71.5	4.4	348	4	US-09-252-991A-23159	Sequence 23159, A
165	74	4.6	953	2	US-09-332-812A-2	Sequence 2, Appli	238	71.5	4.4	348	4	US-09-252-991A-31469	Sequence 31469, A
166	74	4.6	1704	4	US-09-324-867-2	Sequence 2, Appli	239	71.5	4.4	355	4	US-08-669-378-12	Sequence 12, Appli
167	74	4.6	2343	3	US-09-679-279-13	Sequence 13, Appli	240	71.5	4.4	381	4	US-09-935-450-6	Sequence 6, Appli
168	74	4.6	3546	4	US-09-029-213B-25	Sequence 25, Appli	241	71.5	4.4	421	4	US-08-952-899-2	Sequence 2, Appli
169	73.5	4.5	383	1	US-08-464-523B-31	Sequence 31, Appli	242	71.5	4.4	436	3	US-09-338-123-6	Sequence 6, Appli
170	73.5	4.5	408	4	US-09-252-991A-33131	Sequence 33131, A	243	71.5	4.4	443	4		
171	73.5	4.5	436	3	US-08-669-378-4	Sequence 4, Appli	244	71.5	4.4	443	4		
172	73.5	4.5	503	4	US-09-562-737-68	Sequence 68, Appli	245	71.5	4.4	443	4		
173	73.5	4.5					246	71.5	4.4				

247	71.5	4.4	562	3	US-09-211-704A-4	Sequence 4, Appli	320	70.5	4.4	353	3	US-08-482-212-2	Sequence 2, Appli
248	71.5	4.4	567	3	US-09-489-039A-10840	Sequence 10840, A	321	70.5	4.4	353	3	US-08-471-045-55	Sequence 55, Appl
249	71.5	4.4	576	3	US-09-347-801-19	Sequence 19, Appl	322	70.5	4.4	353	3	US-08-469-712A-55	Sequence 55, Appl
250	71.5	4.4	576	3	US-09-347-801-19	Sequence 19, Appl	323	70.5	4.4	353	3	US-08-999-927-2	Sequence 2, Appli
251	71.5	4.4	663	1	US-08-441-139-7	Sequence 7, Appli	324	70.5	4.4	353	3	US-08-999-927-6	Sequence 6, Appli
252	71.5	4.4	857	4	US-09-275-252A-11	Sequence 11, Appl	325	70.5	4.4	353	3	US-08-461-819-2	Sequence 2, Appli
253	71.5	4.4	860	4	US-09-540-236-2184	Sequence 2184, Ap	326	70.5	4.4	353	4	US-08-461-819-6	Sequence 6, Appli
254	71.5	4.4	877	4	US-09-252-991A-25547	Sequence 25547, A	327	70.5	4.4	353	4	US-08-468-910-55	Sequence 55, Appl
255	71.5	4.4	1019	4	US-09-543-681A-4447	Sequence 4447, Ap	328	70.5	4.4	353	4	US-08-761-907-55	Sequence 55, Appl
256	71.5	4.4	1024	4	US-09-563-737-48	Sequence 48, Appl	329	70.5	4.4	353	4	US-09-872-702-13	Sequence 13, Appl
257	71.5	4.4	1447	3	US-09-041-886-25	Sequence 25, Appli	330	70.5	4.4	353	4	PCT-US94-08806-19	Sequence 19, Appl
258	71.5	4.4	1447	3	PCT-US94-05277-2	Sequence 2, Appli	331	70.5	4.4	353	5	PCT-US94-08806-29	Sequence 29, Appl
259	71.5	4.4	1596	4	US-09-328-352-5542	Sequence 5542, Ap	332	70.5	4.4	353	5	PCT-US95-01823-2	Sequence 2, Appli
260	71.5	4.4	198	4	US-09-543-681A-7727	Sequence 7727, Ap	333	70.5	4.4	353	5	PCT-US95-01823-6	Sequence 6, Appli
261	71.5	4.4	246	4	US-09-252-991A-30011	Sequence 30011, A	334	70.5	4.4	353	5	PCT-US95-14932-4	Sequence 4, Appli
262	71.5	4.4	397	1	US-07-956-697B-5	Sequence 5, Appli	335	70.5	4.4	353	5	PCT-US95-14932-5	Sequence 5, Appli
263	71.5	4.4	397	1	US-08-263-098-5	Sequence 5, Appli	336	70.5	4.4	353	5	PCT-US95-16626-4	Sequence 4, Appli
264	71.5	4.4	398	4	US-09-107-532A-3810	Sequence 3810, Ap	337	70.5	4.4	353	5	PCT-US95-16626-6	Sequence 6, Appli
265	71.5	4.4	451	4	US-09-252-991A-32664	Sequence 32664, A	338	70.5	4.4	353	5	US-08-669-378-2	Sequence 2, Appli
266	71.5	4.4	462	4	US-08-630-915A-38	Sequence 38, Appl	339	70.5	4.4	411	2	US-08-491-835-4	Sequence 4, Appli
267	71.5	4.4	480	3	US-09-108-020-6	Sequence 6, Appli	340	70.5	4.4	411	3	US-08-946-092A-4	Sequence 4, Appli
268	71.5	4.4	514	4	US-09-266-965-116	Sequence 116, App	341	70.5	4.4	441	3	US-09-172-062-4	Sequence 4, Appli
269	71.5	4.4	662	3	US-09-232-191-11	Sequence 11, Appl	342	70.5	4.4	441	5	PCT-US94-00685-4	Sequence 4, Appli
270	71.5	4.4	662	3	US-09-232-200-96	Sequence 96, Appl	343	70.5	4.4	441	5	US-09-504-358-2	Sequence 2, Appli
271	71.5	4.4	662	3	US-09-232-200-96	Sequence 96, Appl	344	70.5	4.4	458	4	US-09-954-314-2	Sequence 2, Appli
272	71.5	4.4	662	4	US-09-232-197-11	Sequence 11, Appl	345	70.5	4.4	513	4	US-08-178-477B-32	Sequence 32, Appl
273	71.5	4.4	662	4	US-09-232-201-11	Sequence 11, Appl	346	70.5	4.4	513	4	US-09-304-121-2	Sequence 2, Appli
274	71.5	4.4	662	4	US-09-232-201-11	Sequence 11, Appl	347	70.5	4.4	529	4	US-09-107-532A-6689	Sequence 6689, Ap
275	71.5	4.4	662	4	US-09-232-195-96	Sequence 96, Appl	348	70.5	4.4	529	4	Sequence 594, App	
276	71.5	4.4	662	4	US-09-232-195-96	Sequence 96, Appl	349	70.5	4.4	648	4	US-08-867-941-25	Sequence 25, Appl
277	71.5	4.4	689	3	US-09-232-200-73	Sequence 73, Appl	350	70.5	4.4	702	3	US-08-613-009A-9	Sequence 9, Appli
278	71.5	4.4	689	4	US-09-232-197-73	Sequence 73, Appl	351	70.5	4.4	702	3	US-08-074-658-25	Sequence 25, Appl
279	71.5	4.4	689	4	US-09-232-201-73	Sequence 73, Appl	352	70.5	4.4	702	4	US-08-778-5708-11	Sequence 11, Appl
280	71.5	4.4	689	4	US-09-232-201-73	Sequence 73, Appl	353	70.5	4.4	702	4	US-09-059-584-11	Sequence 11, Appl
281	71.5	4.4	947	4	US-09-252-991A-21398	Sequence 21398, A	354	70.5	4.4	706	4	US-09-059-584-46	Sequence 46, Appl
282	71.5	4.4	1118	3	US-09-379-523-3	Sequence 3, Appli	355	70.5	4.4	783	4	US-09-513-783A-176	Sequence 176, App
283	70.5	4.4	253	4	US-09-328-352-8134	Sequence 8134, Ap	356	70.5	4.4	829	1	US-08-346-455B-34	Sequence 34, Appl
284	70.5	4.4	273	4	US-09-134-001C-4878	Sequence 4878, Ap	357	70.5	4.4	829	3	US-08-977-221-34	Sequence 34, Appl
285	70.5	4.4	326	2	US-08-997-080-43	Sequence 43, Appl	358	70.5	4.4	829	3	US-09-483-831B-34	Sequence 34, Appl
286	70.5	4.4	326	2	US-08-997-362-43	Sequence 43, Appl	359	70.5	4.4	829	5	PCT-US95-06613-34	Sequence 34, Appl
287	70.5	4.4	326	3	US-08-873-970-43	Sequence 43, Appl	360	70.5	4.4	829	5	US-08-346-455B-69	Sequence 69, Appl
288	70.5	4.4	326	3	US-09-095-855-43	Sequence 43, Appl	361	70.5	4.4	915	1	US-08-977-221-69	Sequence 69, Appl
289	70.5	4.4	326	3	US-08-705-347A-43	Sequence 43, Appl	362	70.5	4.4	915	5	PCT-US95-06613-69	Sequence 69, Appl
290	70.5	4.4	326	4	US-09-324-542-43	Sequence 43, Appl	363	70.5	4.4	915	5	US-09-483-831B-69	Sequence 69, Appl
291	70.5	4.4	326	4	US-09-205-426-43	Sequence 43, Appl	364	70.5	4.4	990	4	US-03-252-991A-22792	Sequence 2, Appli
292	70.5	4.4	326	4	US-09-200-643-43	Sequence 43, Appl	365	70.5	4.4	1382	2	US-08-717-715-2	Sequence 7, Appli
293	70.5	4.4	326	3	US-08-875-533-37	Sequence 37, Appl	366	70.5	4.4	1382	4	US-08-457-040B-7	Sequence 12, Appl
294	70.5	4.4	332	3	US-08-875-533-1	Sequence 1, Appli	367	70.5	4.4	1698	3	US-09-315-793-12	Sequence 70, Appl
295	70.5	4.4	332	3	US-08-875-533-2	Sequence 2, Appli	368	70.5	4.4	228	3	US-09-338-907-70	Sequence 70, Appl
296	70.5	4.4	332	3	US-08-875-533-3	Sequence 3, Appli	369	70.5	4.3	228	4	US-09-218-207-70	Sequence 70, Appl
297	70.5	4.4	332	3	US-08-875-533-4	Sequence 4, Appli	370	70.5	4.3	231	4	US-09-489-039A-8999	Sequence 8999, Ap
298	70.5	4.4	332	3	US-08-875-533-5	Sequence 5, Appli	371	70.5	4.3	231	4	US-09-543-681A-4642	Sequence 4642, Ap
299	70.5	4.4	332	3	US-08-875-533-6	Sequence 6, Appli	372	70.5	4.3	266	4	US-09-543-681A-6946	Sequence 6946, Ap
300	70.5	4.4	332	3	US-08-875-533-7	Sequence 7, Appli	373	70.5	4.3	322	4	US-08-345-236B-67	Sequence 67, Appl
301	70.5	4.4	332	3	US-08-875-533-8	Sequence 8, Appli	374	70.5	4.3	344	4	US-08-996-306-4	Sequence 4, Appli
302	70.5	4.4	332	3	US-08-875-533-9	Sequence 9, Appli	375	70.5	4.3	353	3	US-09-338-907-4	Sequence 4, Appli
303	70.5	4.4	332	3	US-08-875-533-10	Sequence 10, Appl	376	70.5	4.3	353	4	US-09-218-207-4	Sequence 5, Appli
304	70.5	4.4	332	3	US-08-875-533-11	Sequence 11, Appl	377	70.5	4.3	353	4	US-08-996-306-5	Sequence 5, Appli
305	70.5	4.4	332	3	US-08-875-533-22	Sequence 22, Appl	378	70.5	4.3	364	2	US-09-318-907-5	Sequence 5, Appli
306	70.5	4.4	332	3	US-08-875-533-66	Sequence 66, Appl	379	70.5	4.3	364	3	US-09-218-207-5	Sequence 5, Appli
307	70.5	4.4	332	3	US-08-875-533-66	Sequence 66, Appl	380	70.5	4.3	364	4	US-09-252-991A-29674	Sequence 29674, A
308	70.5	4.4	332	5	PCT-US95-03776-25	Sequence 25, Appl	381	70.5	4.3	409	4	US-09-134-001C-4302	Sequence 4302, Ap
309	70.5	4.4	333	1	US-08-330-517-2	Sequence 2, Appli	382	70.5	4.3	430	4	US-09-252-232C-29	Sequence 29, Appl
310	70.5	4.4	333	1	US-08-347-029-4	Sequence 4, Appli	383	70.5	4.3	442	3	US-09-086-663A-83	Sequence 83, Appl
311	70.5	4.4	333	1	US-08-388-779A-2	Sequence 2, Appli	384	70.5	4.3	451	4	US-09-198-452A-744	Sequence 744, App
312	70.5	4.4	333	1	US-08-484-246-1	Sequence 1, Appli	385	70.5	4.3	561	4	US-09-640-419C-23	Sequence 23, Appl
313	70.5	4.4	333	1	US-08-591-070A-2	Sequence 2, Appli	386	70.5	4.3	604	3	US-09-000-145-1	Sequence 1, Appli
314	70.5	4.4	333	1	US-08-413-803-25	Sequence 25, Appl	387	70.5	4.3	620	3	US-09-543-681A-6258	Sequence 6258, Ap
315	70.5	4.4	333	1	US-08-321-488A-25	Sequence 25, Appl	388	70.5	4.3	641	4	US-09-328-352-7492	Sequence 7492, Ap
316	70.5	4.4	333	2	US-08-414-161B-2	Sequence 4, Appli	389	70.5	4.3	761	4	US-08-380-182-19	Sequence 19, Appl
317	70.5	4.4	333	2	US-08-457-254-4	Sequence 6, Appli	390	70.5	4.3	863	2	US-08-380-182-20	Sequence 20, Appl
318	70.5	4.4	333	2	US-08-457-254-6	Sequence 2, Appli	391	70.5	4.3	863	2		
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QY 70 IVLIDALRDDDFVFGSK-----GVKEMPYYTTL-----VEKGASHSFVAEAKPPTVT 115
Db 72 IVLIDALRDFDAQOHSHVPREPVSLPFLGKLSLQRIEIQPHARLYRSQVDPPTTT 131
QY 116 MPRIKALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIYFYGDET 165
Db 132 MORKALTTGSLPFIIDAGSNFASHAIVEDNLIKQLTSAGKRVVFMGDDT 181

RESULT 2
US-09-252-991A-21605
; Sequence 21605, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21605
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21605

Query Match 10.5%; Score 170; DB 4; Length 287;
Best Local Similarity 22.9%; Pred. No. 4e-11;
Matches 67; Conservative 48; Mismatches 117; Indels 60; Gaps 10;

QY 41 GAEPAPESAGASSNWTLP-----PPLFSKVIVILDALRDDDFVFGSKGVKEMPYYTTL 96
Db 2 GARPPSP-----AAAPHRRIPRMHVDVILLDGLNH-----SVARDCMHLQAL 46
QY 97 VEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGFVDVIRNLNSPALLEDVIRQAKAAG- 155
Db 47 CGAGRCQSYRLECELPISRLPYECILTGVPIDSGILHNDVVRLSQCSLPHYARAAGL 106
QY 156 -----KRIVF-----YGDETWKLFPKHVEVDGTTSPVSDYTEVDNNV 195
Db 107 STAAAYHWVSELYNEAPDPARDRTDSDALPIQRGH-----FYWSDHYP-DSHL 156
QY 196 TRHLDKVLKRGDWDLILHLVGLDHTCHISGPNPLIGQKLSMDSVLMK-IHTSLQSK 254
Db 157 FADAESLRHAPNFMLVHSMNIDDAHGHGLASPAYRNAARRADALLSEYLHQLAAGY 216
QY 255 RETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLILISAFERKPGDIRHP 306
Db 217 Q-----VAITADHGMNEDRSHGILEBEREVFLFVFGDAFSS--DDLAQP 259

RESULT 3
US-09-540-236-2033
; Sequence 2033, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2033
; LENGTH: 275
; TYPE: PRT
; ORGANISM: M.catarrhalis

US-09-540-236-2033

Query Match 9.2%; Score 148; DB 4; Length 275;
Best Local Similarity 23.0%; Pred. No. 1.4e-08;
Matches 58; Conservative 45; Mismatches 119; Indels 30; Gaps 8;

QY 66 SKVVIVILDALRDDDFVFGSKGVKEMPYYTTLVEKGASHSFVAEAKPPTVTMPRIKALMTG 125
Db 9 NKVILVLDGLNADV-----GLTCMGFLQALCEQHAKAYKLCCELPISRLPYECILTG 63
QY 126 SLPGFVDVIRNLNSPALLEDV-----IROAKAAGKRIYFYGDETWVK-----LFPKHVE 176
Db 64 VRFTDSGIYHQNIRLSKEKSVFYNCIQSNKYTAAAYVWISLYNRSFPQAFDRHTND 123
QY 177 YDGTTSF--FVSDYTEVDNNV---THLDKVLKRGDWDLILHLVGLDHTCHISGNSPL 231
Db 124 SSLPIQFGHFYDDAYFDSHLEFDDADHLRKIYRP---DFLLVHSMNIDDAHGHGLASPAY 180
QY 232 IGQKLSMDSVLMK-IHTSLQSKERETPLNLLVLCGDHGMSETGSHGASSTEEVNTPLI 290
Db 181 YRNAARRADMLLSYINLWLDGQY-----LIIVTSDHGMNDSLHGGNLIEREVPFY 233
QY 291 LISSAFERKPGD 302
Db 234 TIGRFTNKMD 245

RESULT 4

US-09-014-969-19
; Sequence 19, Application US/09014969
; Patent No. 5965397
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallee, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,969
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-014-969-19

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 2, 2004, 16:26:33 ; Search time 16 Seconds
(without alignments)
1863.711 Million cell updates/sec

Title: US-10-036-150-45
Perfect score: 1617
Sequence: 1 MRLSGTFAITCCVAIEVLGI.....LISSAFERKPGDIRHPKHVQ 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : PIR⁷⁸:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	634.5	39.2	758	2 S62432	major facilitator
2	590	36.5	897	2 G84613	hypothetical prote
3	524	32.4	795	2 T21487	hypothetical prote
4	508.5	31.4	830	2 S50810	probable membrane
5	490.5	30.3	880	2 T02245	hypothetical prote
6	414	25.6	918	2 T40030	hypothetical prote
7	387	23.9	1017	2 S64782	probable membrane
8	347.5	21.5	905	2 A87794	protein C27A12.9 (
9	172.5	10.7	935	2 T40715	hypothetical prote
10	170	10.5	919	2 S37786	hypothetical prote
11	163.5	10.1	269	2 D81344	hypothetical prote
12	157	9.7	289	2 E83240	probable phosphodi
13	152.5	9.4	429	2 T33724	probable phosphodi
14	151	9.3	485	2 T40657	probable phosphodi
15	147	9.1	479	2 T03293	probable phosphodi
16	139	8.6	461	2 T09933	probable phosphodi
17	138	8.5	477	1 A59391	probable phosphodi
18	134	8.3	457	2 T09932	probable phosphodi
19	134	8.3	456	2 T09931	probable phosphodi
20	130	8.0	477	1 A59390	probable phosphodi
21	122.5	7.6	451	2 F87407	probable phosphodi
22	122	7.5	433	2 B82537	probable phosphodi
23	114	7.1	370	2 T10552	hypothetical prote
24	114	7.1	825	2 T46311	hypothetical prote
25	114	7.1	963	2 A57238	iron-responsive el
26	111.5	6.9	369	2 A75091	phosphonoacetate h
27	111.5	6.9	905	1 A27410	nucleotide diphosp
28	111	6.9	885	1 A55453	nucleotide diphosp
29	110.5	6.8	434	2 P96958	ap superfamily [im

30	108.5	6.7	520	2 D83845	hypothetical prote
31	101	6.2	743	2 S19437	hypothetical prote
32	101	6.2	925	1 A39216	nucleotide diphosp
33	96.5	6.0	2109	1 ZLVN	genome polyprotein
34	96	5.9	561	2 T05545	pollen-specific pr
35	95.5	5.9	513	2 A38193	phosphoprotein pho
36	94.5	5.8	388	2 F75162	cryptophan synthas
37	92	5.7	461	2 B90555	ABC transporter xy
38	92	5.7	521	2 C75320	glycyl-tRNA synthet
39	92	5.7	638	2 A33505	somatotropin recep
40	91.5	5.7	629	2 T22691	hypothetical prote
41	91.5	5.7	853	2 B81277	hypothetical prote
42	90.5	5.6	327	2 G89842	hypothetical prote
43	90.5	5.6	422	2 AB1252	hypothetical prote
44	90.5	5.6	826	2 B36203	pyrophosphatase ho
45	90.5	5.6	826	2 B36203	iron-responsive el
46	90.5	5.6	952	2 B57238	iron-responsive el
47	90	5.6	231	2 AD0949	hypothetical prote
48	90	5.6	634	2 S33339	somatotropin recep
49	89.5	5.5	291	2 AB1163	flagellar hook-ass
50	89.5	5.5	291	2 AB1163	flagellar hook-ass
51	89.5	5.5	300	1 H70557	probable acyl-CoA
52	89.5	5.5	510	2 S42705	probable phosphogl
53	89.5	5.5	604	2 H72712	probable RNase L i
54	89	5.5	359	1 A31425	uracil-DNA glycosy
55	89	5.5	700	2 A83434	conserved hypotet
56	89	5.5	891	2 T19915	hypothetical prote
57	88.5	5.5	258	1 OYECFH	imidazoleglycerol-
58	88.5	5.5	258	2 B90382	imidazoleglycerol-
59	88.5	5.5	258	2 H85827	imidazoleglycerol-
60	88.5	5.5	424	2 B95964	probable phosphono
61	88.5	5.5	802	2 C95136	conserved domain p
62	88.5	5.5	828	2 B98004	hypothetical prote
63	88	5.4	427	2 F83984	acetylornithine de
64	88	5.4	453	2 T16795	hypothetical prote
65	88	5.4	660	2 AD0661	invasin-like prote
66	87.5	5.4	1216	2 A28822	1-phosphatidylinos
67	87	5.4	314	2 A39374	renilla-luciferin
68	87	5.4	875	1 A57080	cell surface antig
69	86.5	5.3	365	2 S36807	cytochrome P450 71
70	86.5	5.3	476	2 A46118	myosin-binding pro
71	86.5	5.3	519	2 T46163	hypothetical prote
72	86.5	5.3	527	2 E90740	probable enzyme li
73	86.5	5.3	527	2 G85590	probable enzyme yb
74	86.5	5.3	527	2 G64818	probable membrane
75	86	5.3	485	2 T64157	hypothetical prote
76	86	5.3	496	2 T44987	aldehyde dehydroge
77	86	5.3	637	2 B83052	bnak protein PA476
78	85.5	5.3	389	2 T43927	tryptophan synthas
79	85.5	5.3	390	2 T16746	hypothetical prote
80	85.5	5.3	913	2 T46339	hypothetical prote
81	85	5.3	378	2 B87304	N-acetylglucosamin
82	85	5.3	510	2 AH1381	phosphoglycerate m
83	85	5.3	510	2 AH1750	phosphoglycerate m
84	85	5.3	511	2 D97753	alkaline protease
85	85	5.3	677	2 S33608	somatotropin-bindi
86	85	5.3	906	2 G75362	acconitate hydratase
87	85	5.3	1098	2 S36868	alpha,alpha-trehal
88	85	5.3	1696	2 T00057	hypothetical prote
89	84.5	5.2	381	2 E72255	conserved hypotet
90	84.5	5.2	453	1 A59389	probable phosphodi
91	84.5	5.2	480	2 D75053	hypothetical prote
92	84.5	5.2	545	2 H83079	hypothetical prote
93	84.5	5.2	592	2 T15600	hypothetical prote
94	84.5	5.2	642	2 T41690	conserved hypotet
95	84.5	5.2	810	2 S75931	hypothetical prote
96	84	5.2	374	2 S75459	hypothetical prote
97	84	5.2	416	1 ITSH	alpha-1-antitrypsi
98	84	5.2	479	2 D30411	synapsin IIb - rat
99	84	5.2	585	2 C36858	G3R protein - vari
100	84	5.2	585	2 T28622	hypothetical prote
101	84	5.2	586	2 C30411	synapsin Iia - rat
102	83.5	5.2	336	1 S28412	carbonate dehydrat

103	83.5	5.2	349	2	T15082	hypothenical prote	176	79	4.9	637	2	JC5608	dnak-type molecula
104	83.5	5.2	482	2	C90067	hypothenical prote	177	79	4.9	638	2	S12136	smatotropin recep
105	83	5.1	331	1	S48675	carbonate dehydrat	178	79	4.9	907	2	T04820	aconitate hydrat
106	83	5.1	357	2	S73851	hypothenical prote	179	78.5	4.9	314	2	G69818	CMP-binding factor
107	83	5.1	400	2	B90001	hypothenical prote	180	78.5	4.9	501	2	B86351	protein disulfide-
108	83	5.1	472	2	AD1609	6-phosphogluconate	181	78.5	4.9	523	2	B71985	hypothenical prote
109	83	5.1	472	2	AH1246	6-phosphogluconate	182	78.5	4.9	545	2	S58370	carboxylesterase (
110	83	5.1	593	2	C83821	glycyl-tRNA synthe	183	78.5	4.9	549	2	S53427	protein-tyrosine-p
111	83	5.1	2175	1	S03170	homeotic protein c	184	78.5	4.9	600	2	A82043	inner membrane cop
112	83	5.1	3157	2	B70969	probable PPE prote	185	78.5	4.9	604	2	E75119	hypothenical prote
113	82.5	5.1	368	2	AF1185	alanine racemase h	186	78.5	4.9	608	2	AC0798	probable sodium/su
114	82.5	5.1	422	2	AH1614	weakly pyrophospha	187	78.5	4.9	609	2	S72845	H+-transporting tw
115	82.5	5.1	511	2	D71687	alkaline proteinase	188	78.5	4.9	656	1	A55574	protein-tyrosine-p
116	82.5	5.1	562	2	H70688	hypothenical prote	189	78.5	4.9	665	2	F97032	beta-glucosidase f
117	82.5	5.1	898	2	T10101	aconitate hydrat	190	78.5	4.9	674	2	F83794	ABC transporter (A
118	82.5	5.1	898	2	B84471	cytoplasmic aconit	191	78.5	4.9	761	2	G70393	conserved hypotet
119	82.5	5.1	1398	2	T28159	pyrolysins (EC 3.4.	192	78.5	4.9	775	2	S65769	maltooligosyl treh
120	82	5.1	322	2	A82618	hypothenical prote	193	78.5	4.9	804	2	A96494	protein F/F22.16 (
121	82	5.1	972	2	T49773	related to actin-i	194	78.5	4.9	848	2	G86708	aconitate hydrat
122	82	5.1	1458	2	S36014	dynein heavy chain	195	78.5	4.9	1108	2	A55915	guanylate cyclase
123	82	5.1	1386	2	S28353	probable polyketid	196	78.5	4.9	1173	1	A53430	1-phosphatidylino
124	81.5	5.0	352	2	A81136	probable anthranil	197	78.5	4.9	1216	2	A28821	2-phosphatidylino
125	81.5	5.0	521	2	A33264	phosphoprotein pho	198	78.5	4.9	1654	2	A12067	two-component sens
126	81.5	5.0	521	2	A31257	phosphoprotein pho	199	78	4.8	242	2	AB1184	B. subtilis NagB p
127	81.5	5.0	525	2	F81017	YhbX/YhjW/Yjlp/Yjd	200	78	4.8	230	2	AB2769	conserved hypotet
128	81.5	5.0	548	2	G70807	probable fadB9 pr	201	78	4.8	336	1	S61882	carbonate dehydrat
129	81.5	5.0	601	2	F83471	hypothenical prote	202	78	4.8	336	2	E84311	histidinol-phospha
130	81.5	5.0	795	1	S73830	endopeptidase La (203	78	4.8	364	2	D97549	hypothenical prote
131	81.5	5.0	940	2	B18852	probable type III	204	78	4.8	432	2	T01925	hypothenical prote
132	81.5	5.0	987	2	A75496	conserved hypotet	205	78	4.8	437	2	JC4929	transcription fact
133	81.5	5.0	1467	2	G72352	hypothenical prote	206	78	4.8	465	2	H90508	cobyrinic acid synth
134	81	5.0	381	2	G72352	hypothenical prote	207	78	4.8	497	2	T15872	hypothenical prote
135	81	5.0	490	2	F70146	glutamate-tRNA lig	208	78	4.8	532	2	S54571	probable membrane
136	81	5.0	585	1	F64159	hypothetical prote	209	78	4.8	619	2	AI3336	potassium/proton a
137	81	5.0	626	1	A48648	acetylacrate synth	210	78	4.8	900	2	AI1279	aconitate hydrat
138	81	5.0	1469	2	T19168	hypothenical prote	211	78	4.8	1010	1	AJHUPR	phosphoribosylamin
139	81	5.0	2078	2	T25400	hypothenical prote	212	77.5	4.8	272	2	B95852	conserved hypotet
140	80.5	5.0	258	1	OYEBHF	cyclase HisF - Sal	213	77.5	4.8	273	2	T34672	probable gntR fami
141	80.5	5.0	258	1	AI0764	cyclase HisF [impo	214	77.5	4.8	293	2	T37992	probable tricarbox
142	80.5	5.0	281	2	F97844	hypothenical prote	215	77.5	4.8	331	2	AC0842	glycine betaine-bi
143	80.5	5.0	395	2	H75457	hypothenical prote	216	77.5	4.8	341	2	H90797	probable tellurium
144	80.5	5.0	491	2	AH3415	AMP nucleosidase (217	77.5	4.8	385	2	A85607	hypothenical prote
145	80.5	5.0	505	2	C90569	hypothenical prote	218	77.5	4.8	408	2	AH3269	dihydroliboamide S
146	80.5	5.0	537	2	H64241	arginine-tRNA liga	219	77.5	4.8	451	2	H69006	DNA-directed RNA p
147	80.5	5.0	751	2	T30154	hypothenical prote	220	77.5	4.8	478	2	JC4940	synapsin IIB - mou
148	80.5	5.0	1036	2	S22383	axinin 1 precursor	221	77.5	4.8	503	2	I84771	probable zinc meta
149	80.5	5.0	1741	2	T13610	parallel sister ch	222	77.5	4.8	517	2	T20658	probable zinc meta
150	80	4.9	250	2	T08908	hypothenical prote	223	77.5	4.8	521	1	S35067	phosphoprotein pho
151	80	4.9	397	2	H72491	probable tyrosine	224	77.5	4.8	521	1	A56968	phosphoprotein pho
152	80	4.9	424	2	D89892	dihydrocorotase [im	225	77.5	4.8	540	2	T32230	hypothenical prote
153	80	4.9	1813	2	T30564	resistance protein	226	77.5	4.8	545	2	S58980	carboxylesterase (
154	79.5	4.9	270	2	G72390	dihydrocorotase deh	227	77.5	4.8	545	2	S58979	carboxylesterase (
155	79.5	4.9	276	2	G75358	hypothenical prote	228	77.5	4.8	545	2	S58974	carboxylesterase (
156	79.5	4.9	333	2	JC7139	endo-1,4-beta-xyla	229	77.5	4.8	545	2	S58975	carboxylesterase (
157	79.5	4.9	397	2	T35880	hypothenical prote	230	77.5	4.8	545	2	S58975	carboxylesterase (
158	79.5	4.9	416	2	A87093	probable membrane	231	77.5	4.8	545	2	S58982	carboxylesterase (
159	79.5	4.9	545	2	D90159	hypothenical prote	232	77.5	4.8	545	2	S58983	carboxylesterase (
160	79.5	4.9	560	1	F69059	arginine-tRNA liga	233	77.5	4.8	545	2	S58976	carboxylesterase (
161	79.5	4.9	844	2	T37079	DNA ligase (ATP) (234	77.5	4.8	545	2	S58968	carboxylesterase (
162	79.5	4.9	986	2	T03760	pallulanase (EC 3.	235	77.5	4.8	545	2	S58981	carboxylesterase (
163	79.5	4.9	1072	2	A86827	hypothenical prote	236	77.5	4.8	567	2	E35928	hypothenical prote
164	79.5	4.9	1090	2	A41696	regulatory protein	237	77.5	4.8	579	2	F81711	conserved hypotet
165	79.5	4.9	1257	2	T01020	hypothenical prote	238	77.5	4.8	609	2	F70512	probable ATPase -
166	79.5	4.9	2535	2	T02648	hypothenical prote	239	77.5	4.8	656	1	JC4263	protein-tyrosine-p
167	79	4.9	247	2	A80545	probable transmem	240	77.5	4.8	808	1	T04982	dynamitin-like prote
168	79	4.9	368	2	AEL1543	alanine racemase h	241	77.5	4.8	842	2	F97850	DNA-directed DNA p
169	79	4.9	372	2	T01600	hypothenical prote	242	77.5	4.8	945	2	C96760	probable sucrose s
170	79	4.9	410	2	D70599	hypothenical prote	243	77.5	4.8	1021	2	T42634	connectin/titin -
171	79	4.9	416	2	S21097	alpha-1-antitrypsi	244	77.5	4.8	1423	2	A49206	exo-beta-D-fructos
172	79	4.9	427	2	A40735	TGF beta homolog d	245	77	4.8	175	2	H69403	probable lipoprote
173	79	4.9	511	2	T46865	phosphoglycerate m	246	77	4.8	211	2	H69403	conserved hypotet
174	79	4.9	610	2	A80459	hypothenical prote	247	77	4.8	280	2	AD2248	hypothenical prote
175	79	4.9	632	2	G69306	NADH oxidase (noxB	248	77	4.8	372	2	T50014	trehalose-6-phosph

249	77	4.8	403	2	S58345	B2F-1 transcriptio	322	75.5	4.7	725	2	AB1187	conserved hypothet
250	77	4.8	564	2	T43298	transcription fact	323	75.5	4.7	820	2	T14879	hypothetical prote
251	77	4.8	631	2	R31203	interferon-regulat	324	75.5	4.7	898	2	T21821	hypothetical prote
252	77	4.8	878	1	A40091	interleukin-3 rece	325	75.5	4.7	932	2	D97351	sensor protein Kcp
253	77	4.8	1080	2	T03964	probable ubiquitin	326	75.5	4.7	968	2	G86857	isoleucine-tRNA li
254	77	4.8	1135	2	T03561	Scythe protein - A	327	75.5	4.7	982	2	G82452	hypothetical prote
255	77	4.8	1643	1	RRWGNV	genome polypeptide	328	75.5	4.7	982	2	S58881	mut8 [acetyl-homol
256	77	4.8	2256	2	AD1018	large repetitive p	329	75.5	4.7	2504	1	A57788	enoyl-l-acyl-carrie
257	76.5	4.7	295	2	F72777	hypothetical prote	330	75.5	4.7	3283	2	AC1018	large repetitive p
258	76.5	4.7	332	2	H66830	catabolite control	331	75	4.6	142	2	B84934	50S ribosomal prot
259	76.5	4.7	342	2	E82955	TonB protein PA53	332	75	4.6	244	2	A90786	probable synthetas
260	76.5	4.7	430	2	F81698	3-deoxy-manno-octu	333	75	4.6	244	2	G85645	probable synthetas
261	76.5	4.7	457	2	F71172	hypothetical prote	334	75	4.6	359	2	T01275	hypothetical prote
262	76.5	4.7	478	2	S06987	nitrogenase (EC 1.	335	75	4.6	364	2	S34355	peroxidase (EC 1.1
263	76.5	4.7	544	2	B40122	carboxylesterase (336	75	4.6	407	2	B84993	phosphopentomutase
264	76.5	4.7	569	2	A97638	urease alpha chain	337	75	4.6	413	2	I56481	alpha 1-proteinase
265	76.5	4.7	569	2	AG2871	urease alpha subun	338	75	4.6	440	2	I61183	transcription fact
266	76.5	4.7	573	1	S33212	INDA1 protein - fu	339	75	4.6	453	2	H97373	hypothetical prote
267	76.5	4.7	585	2	D35419	RhBC rhizobactin s	340	75	4.6	466	2	T11884	RVS167 protein hom
268	76.5	4.7	585	2	T46816	RhBC protein limpo	341	75	4.6	469	2	A81836	probable 3-isoprop
269	76.5	4.7	710	1	C43497	early transcriptio	342	75	4.6	469	2	G81128	3-isopropylmalate
270	76.5	4.7	710	1	I42537	early transcriptio	343	75	4.6	485	2	AF3106	glutamyl-tRNA synt
271	76.5	4.7	710	2	T37334	VERP, 82K subunit	344	75	4.6	488	2	F98180	glutamyl-tRNA synt
272	76.5	4.7	998	2	C75489	conserved hypothet	345	75	4.6	501	2	C82414	aminopeptidase VCA
273	76.5	4.7	1064	2	C86795	carbamoylphosphate	346	75	4.6	536	2	G64752	xylan 1,4-beta-xyl
274	76.5	4.7	1274	2	S55050	cardiac myosin-bin	347	75	4.6	553	2	A69830	arginyl-tRNA synth
275	76.5	4.7	1295	2	T21720	hypothetical prote	348	75	4.6	711	2	T05321	arginine decarboxy
276	76.5	4.7	1383	2	T13082	guanine nucleotide	349	75	4.6	976	2	A36355	protein-tyrosine k
277	76	4.7	206	2	T36643	probable integral	350	75	4.6	1052	2	AG3206	AcR5/AcrD/AcrF fam
278	76	4.7	244	1	A64843	hypothetical prote	351	75	4.6	1086	2	JC6079	chitin synthase (B
279	76	4.7	322	2	H70462	quinolinate synthe	352	75	4.6	1244	2	T19068	hypothetical prote
280	76	4.7	345	2	T02798	hypothetical prote	353	75	4.6	1250	2	T40062	probable nuclear e
281	76	4.7	348	2	T02798	hypothetical prote	354	75	4.6	1338	2	T30565	MAP kinase kinase
282	76	4.7	376	1	T39454	hypothetical prote	355	75	4.6	1391	2	S73652	RNA polymerase bat
283	76	4.7	470	1	E64081	probable rhamnulok	356	75	4.6	3869	2	A48205	All-1 protein +GNE
284	76	4.7	493	2	S50443	probable phosphodi	357	74.5	4.6	233	2	B69900	conserved hypothet
285	76	4.7	511	2	D69675	phosphoglycerate m	358	74.5	4.6	255	2	A86894	30S ribosomal prot
286	76	4.7	514	2	T47556	pyruvate kinase-11	359	74.5	4.6	303	2	AH0082	LysR-family regula
287	76	4.7	616	2	JQ1441	hypothetical 67K p	360	74.5	4.6	366	1	W2WLR1	E2 protein - rhesu
288	76	4.7	638	2	B28176	somatotropin recep	361	74.5	4.6	464	2	B83029	replicative DNA he
289	76	4.7	659	2	F70453	aconitase - Aquife	362	74.5	4.6	467	2	T02238	glucosyl transfera
290	76	4.7	709	2	D82825	conserved hypothet	363	74.5	4.6	473	2	E75097	hypothetical prote
291	76	4.7	805	2	T37787	probable vacuolar	364	74.5	4.6	476	2	AI0080	ADP-heptose syntha
292	76	4.7	822	2	T01622	probable salt-indu	365	74.5	4.6	487	2	A69845	methylnalonaate-sen
293	76	4.7	851	2	T38173	probable phosphati	366	74.5	4.6	504	2	S01074	L-arabinose transp
294	76	4.7	863	2	B71343	probable ribosomal	367	74.5	4.6	504	2	H90954	L-arabinose transp
295	76	4.7	907	2	AD2951	cell division prot	368	74.5	4.6	510	2	F96987	2,3-bisphosphoglyc
296	76	4.7	909	2	G69599	aconitate hydratase	369	74.5	4.6	513	2	S35132	2-isopropylmalate
297	76	4.7	910	2	H98331	cell division prot	370	74.5	4.6	521	2	T32231	hypothetical prote
298	76	4.7	944	2	T38130	probable helicase	371	74.5	4.6	532	2	B87496	protein-export mem
299	76	4.7	956	1	S53237	pyruvate, phosphat	372	74.5	4.6	532	2	L49329	retinoblastoma-ass
300	76	4.7	1068	2	A40285	retinoblastoma-ass	373	74.5	4.6	693	2	D97122	translation IF2, G
301	76	4.7	1165	1	GNLJGL	HIV-1 retropepsin	374	74.5	4.6	693	2	AE3468	diagnalyate cyclas
302	76	4.7	1512	2	T14893	hypothetical prote	375	74.5	4.6	710	1	H36848	early transcriptio
303	76	4.7	2137	2	T05244	hypothetical prote	376	74.5	4.6	710	2	E72164	A8L protein - vari
304	76	4.7	2366	2	S10317	toxin B - Clostrid	377	74.5	4.6	710	2	T28549	hypothetical prote
305	75.5	4.7	222	2	JQ0640	glutamine amidotra	378	74.5	4.6	715	2	S70397	zona pellucida gly
306	75.5	4.7	272	2	B75414	nolhydramine cofact	379	74.5	4.6	903	2	E88221	protein TolH3.2 fi
307	75.5	4.7	278	2	T18887	hypothetical prote	380	74.5	4.6	980	2	T24336	hypothetical prote
308	75.5	4.7	293	2	H99802	conserved hypothet	381	74.5	4.6	987	2	A64474	hypothetical prote
309	75.5	4.7	312	2	H64250	L-lactate dehydrog	382	74.5	4.6	992	2	T38817	hypothetical prote
310	75.5	4.7	332	2	AD2078	transcription regu	383	74.5	4.6	1036	2	AG1326	alpha-mannosidase
311	75.5	4.7	350	2	T33458	hypothetical prote	384	74.5	4.6	1061	2	I49328	retinoblastoma-ass
312	75.5	4.7	512	1	ISAAGS	protein disulfide-	385	74.5	4.6	1104	2	A60999	alpha-amylose (EC
313	75.5	4.7	512	2	A41440	protein disulfide-	386	74.5	4.6	1178	2	S57698	regulatory protein
314	75.5	4.7	545	2	S58978	carboxylesterase (387	74.5	4.6	1254	2	G86379	protein F5A9.24 fi
315	75.5	4.7	545	2	S58978	carboxylesterase (388	74.5	4.6	1493	2	T19751	hypothetical prote
316	75.5	4.7	545	2	S58977	carboxylesterase (389	74.5	4.6	2311	1	TVCHSR	kinase-related pro
317	75.5	4.7	545	2	S58973	carboxylesterase (390	74.5	4.6	3432	1	GNWVUE	genome polypeptide
318	75.5	4.7	567	2	T30799	hypothetical prote	391	74.5	4.6	3432	1	GNWVUE	genome polypeptide
319	75.5	4.7	567	2	T42509	B6R protein - vacc	392	74.5	4.6	26936	1	I38344	titin, cardiac mus
320	75.5	4.7	568	1	A05225	gamma-glutamyltran	393	74	4.6	252	2	T51616	chlorophyll a/b-bi
321	75.5	4.7	669	2	T51220	hypothetical prote	394	74	4.6	284	2	S60250	maB-18 protein (tr

A:Accession: S47129
A:Molecule type: DNA
A:Residues: 1-830 <VAV>
A:Cross-references: EMBL:Z34288; NID:g498992; PID:g498992
R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hinger
submitted to the Protein Sequence Database, September
A:Reference number: S56835
A:Accession: S56835
A:Molecule type: DNA
A:Residues: 1-830 <POH>
A:Cross-references: EMBL:Z49337; NID:gl008208; PID:g498992
R:Pohl, T.M.; Aljinovic, G.
submitted to the Protein Sequence Database, September
A:Reference number: S56793
A:Accession: S56834
A:Molecule type: DNA
A:Residues: 111-830 <TOV>

0005
F.
1995

008209; MIPS:YJL062W
1995

A:Cross-references: EMBL:Z49337; MIPS:YJL062w

C:Genetics:

A:Gene: SGD:LAS21

A:Cross-references: SGD:S0003598

A:Map position: 10L

C:Keywords: transmembrane protein

Query Match 31.4%; Score 508.5; DB 2; Length 830;

Best Local Similarity 38.8%; Pred. No. 3.5e-33;

Matches 119; Conservative 53; Mismatches 110; Indels 25; Gaps 9;

QY 10 TCCTVAIEVLGIATVFLGFFPAPVRSSARAEHGAEPAPPSAGASNNWTLTPPLFVKV 69

DB 7 TCSLCAQLLAILFIAFFPKIVL-----GISKQDPQDRDLQDRP-----FQKLV 55

QY 70 IVLIDALRDDVFGSGVKVMPYTYLVKKGASHSVFAEAKPTVTMPRIKALMTGSLPG 129

DB 56 FVIIDALRSDFLDSQISHFNHVL-NTGEAWGTSFANPFTVLPRLKSIITGSTPS 114

QY 130 FVDVIRN-----LNSPALLE-DSVIRQAKAAGKRIYVYGDVTWVLPFKHFVEY-DGTTSF 183

DB 115 FIDLLNVAQIDISNDLSEHSDWLOFIOHNTIRFGDDTWLKLFPQGFADPTHSF 174

QY 184 FVSIDYTDVNNVTRHLDKVL--KRGDWDILHYGLDHIHISGPNPLIGQKLSMDS 241

DB 175 FVSDFDQVNDVNNVTRNLPFGKLFQEWAGQWVAILHYGLDHIHISGPNPLIGQKLSMDS 234

QY 242 VLMKIHTSLQSKERETPLNLAIVLGDHGMSETSGHSGASSTEEVNTPLILIS---SAPER 298

DB 235 ILKSIYDEV--LEHEDDDTLICVLGDHGMNGLNHHGSSAGETSAGLFLSPKLAQFAR 292

QY 299 KFGDIRH 305

DB 293 PESQVNY 299

RESULT 5

T02245

Hypothetical protein P1.11659.3 - human

C:Species: Homo sapiens (man)

C>Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Nov-1999

C:Accession: T02245

R:Lamerdin, J.E.; McCreedy, P.M.; Skowronski, E.; Adamson, A.W.; Burkhardt-Schultz, K.; G

Christensen, M.; Georgescu, A.; Avila, J.; Liu, S.; Attix, C.; Andreise, T.; Frankel

submitted to the EMBL Data Library, March 1998

A:Authors: Duarte, S.; Lucas, S.; Bruce, R.; Thomas, P.; Quan, G.; Krommiller, B.; Arell

A:Description: Sequence analysis of a human P1 clone containing the XRCC9 DNA repair ge

A:Reference number: Z14637

A:Accession: T02245

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-880 <IAM>

A:Cross-references: EMBL:AC004472; NID:G2984582; PIDN:AAC07985.1; PID:G2984587

C:Genetics:

A:Map position: 9

A:Introns: 89/3; 152/1; 200/1; 241/2; 294/3; 354/3; 435/1; 733/1; 802/1; 871/1

Query Match

Best Local Similarity 30.3%; Score 450.5; DB 2; Length 880;

Matches 115; Conservative 45; Mismatches 92; Indels 35; Gaps 9;

QY 19 GIATVLRGFFPAPVRSSARAEHGA--EPPAPEPSAGASNNWTLTPPP-----LFSKV 69

DB 20 GIALTSGFLTRLELT---NHSSQEPGP-----GSLPMGSGQKPGACWMAFRFRVV 71

QY 70 IVLIDALRDDVFGSGVKVMPYTYLVKKGASHSVFAEAKPTVTMPRIKALMTG 126

DB 72 LVLIDALDFDA-----QFQSHRILETQPHARLYRSQVDPPTTTMORLKALTGS 123

QY 127 LPGFVDVIRNLSNPALEDSVIRQAKAAGKRIYVYGDVTWVLPFKHFVEYDGTTSFVS 166

DB 124 LPTIDAGSNFASHAIVEDNLIKQLTSAGRVVFMGDDTWKDLFPFGAFKAFPPSPNVR 183

QY 187 DYTEVDNNVTRHLDKVLKRGDWDILHYGLDHIHISGPNPLIGQKLSMDSVLMKI 246

DB 184 DLDTVNDGILIEHLPTMTDSGEWDVLAHFLGVHCHGKHGPHPEKAKLSQMDQVIOGL 243

QY 247 HTLSQSKERETPLNLAIVLGDHGMSETSGHSGASSTEEVNTPLILIS 293

DB 244 ---VERLENDT---LLVAGDHGMVTNGDHGDSSELEVSAAFLYS 283

RESULT 6

T40030

Hypothetical protein SPBC27B12.06 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T40030

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A.

submitted to the EMBL Data Library, December 1997

A:Reference number: Z21900

A:Accession: T40030

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-918 <WOO>

A:Cross-references: EMBL:AL021766; PIDN:CAAL6901.1; GSPDB:GN00067; SPDB:SPBC27B12.06

A:Experimental source: strain 972h-; cosmid c27B12

C:Genetics:

A:Gene: SPDB:SPBC27B12.06

A:Map position: 2

Query Match

Best Local Similarity 25.8%; Score 414; DB 2; Length 918;

Matches 105; Conservative 60; Mismatches 121; Indels 38; Gaps 11;

QY 3 LGSSTFATCCVAIEVL-----GIATVLRGFF--PAPVRSSARAEHGAEPAP-EP 53

DB 16 IGWKYIQACIFPAIILISNFYGLKSTGDFLRRALVNLQSLCEN---PPADVREWKNS 72

QY 54 SSNWTLPPPLFSKVIVILIDALRDDVFGSGVKVF-----MPYTYLVKRGASH--SF 105

DB 73 SGCWA--PKIFERAVIVIIDALRYDFLIPYDNSNYHNAFTTPYETSVLHPENSVLIOF 129

QY 106 VAEAKPTVTMPRIKALMTGSLPGFVDVIRNLSNPALEDSVIRQAKAAGKRIYVYGD 165

DB 130 IADA--PTTTSQRLKGLTTSUPTFIDLSNFAGTNIDEDNLLQWKSQDLQVILLGDDT 187

QY 166 WVKLFPKHFE--YDGTTFVSDYTEVDNNVTRHLDKVLKRGDWDILHYGLDHIH 223

DB 188 WDLPHDYLNETLSQAPAFSNFVPLDGHVDNKVQYVFDVIKDNFVLIHLYGVHDVGH 247

QY 224 ISGPNPLIGQKLSMDSVLMKIHTSLQSKERETPLNLAIVLGDHGMSETSGHSGAS 283

DB 248 RLGPDPHTVRDKLNQMDRCVKEMDMLDLS-----TLIVMGDHGMKNHSGDSDPD 300

QY 284 EVNTPLILISS---AFERKPGDI 303

DB 301 EINSVLWYWKETFGYLLKQPGKV 324

RESULT 7

S64782

probable membrane protein YLL031C - Yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein L0929

C:Species: Saccharomyces cerevisiae

C>Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 19-Apr-2002

C:Accession: S64782

R:Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.

submitted to the Protein Sequence Database, May 1996

A:Reference number: S64775

A:Accession: S64782

A:Molecule type: DNA

A:Residues: 1-1017 <DUE>

A:Cross-references: EMBL:Z73136; NID:gl360215; PID:gl360216; GSPDB:GN00012; MIPS:YLL031C

A:Experimental source: strain S288C

C:Genetics: